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FORM PTO-1390 U S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE
(REV 10.95)

ATTORNEY'S DOCKET NUMBER
674537-2002

09/623611
U S. APPLICATION NO. (If known see 37 C F.R. 1 5)

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	(EARLIEST) PRIORITY DATE CLAIMED
PCT/AU99/00136	05 MARCH 1999	06 MARCH 1998

TITLE OF INVENTION: **V-LIKE DOMAIN BINDING MOLECULES**

APPLICANTS FOR DO/EO/US: **Gregory COIA, Maria GALANIS, Peter John HUDSON, Robert Alexander IRVING and Stewart Douglas NUTTALL**

Applicants herewith submit to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
   a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☒ has been transmitted by the International Bureau.
   c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☒ A translation of the International Application into English (35 U.S.C. 371(c)(2)), including 15 sheets of formal drawings and a copy of the International Search Report.
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
   a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☐ have been transmitted by the International Bureau.
   c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☐ An oath or declaration of the inventors (35 U.S.C. 371(c)(4)).
10. ☐ The annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern other document(s) or information included:

11. ☒ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A FIRST preliminary amendment.
    ☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information:

    PCT/ISA/210, PCT/RO/101,

    PCT/IPEA/409,

    References for IDS, Sequence listing (56 sheets)

    1 Page Abstract

EXPRESS MAIL

Mailing Label Number: EL588273756US

Date of Deposit: September 5, 2000

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JMM3023

U.S. APPLICATION NO.(If known, see 37 C.F.R. 1.50) 09/623611 | INTERNATIONAL APPLICATION NO PCT/AU99/00136 | ATTORNEY'S DOCKET NO. 674537-2002

17. ☒ The following fees are submitted: (CALCULATIONS /PTO USE ONLY

Basic National Fee (37 CFR 1.492(a)(1)-(5):

Search Report has been prepared by the EPO or JPO.....$840.00 ($840.00

International preliminary examination fee paid to USPTO (37 CFR 1.482) $700.00

No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2))...$770.00

Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37CFR 1.445(a)(2) paid to USPTO.....$1040.00

International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4).....$96.00

ENTER APPROPRIATE BASIC FEE AMOUNT = **($ 840.00**

Surcharge of **$130.00** for furnishing the oath or declaration later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(e)). ($ /

33 Claims	/Number Filed /	Number Extra	/Rate (
Total Claims	/ 33 - 20 = / 13	/X $18.00	**($ 234.00**
Independent Claims	/ 3- 3 = / 0	/X $78.00	**($ 0.00**
Multiple dependent claim(s) (if applicable)		/+ $260.00	($

TOTAL OF ABOVE CALCULATIONS = ($1,074.00

Reduction by 1/2 for filing by small entity, if applicable. Verified Small Entity (/ statement must also be filed. (Note 37 CFR 1.9, 1.27, 1.28). **($ 0.00/**

SUBTOTAL = **($1,074 .00**

Processing fee of **$130.00** for furnishing the English translation later than (/ ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(f)).+ ($ /

TOTAL NATIONAL FEE = ($1,074.00

Fee for recording the enclosed assignments (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). $40.00 per property + **($ 0.00/** ($ /

TOTAL FEES ENCLOSED = ($1,074.00

(Amount to be: / (refunded /$

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a. ☒ Our check in the amount of $1,074.00 to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account No. 50-0320 in the amount of $_____ to cover the above fees. A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. **50-0320**. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

THOMAS J. KOWALSKI
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745 FIFTH AVENUE
NEW YORK, NEW YORK 10151

Dated: September 5, 2000

SIGNATURE

THOMAS J. KOWALSKI
NAME

32,147
REGISTRATION NUMBER

Form PTO-1390 (REV **10-96**)

JMM3023

09/622014
532 Rec'd PCT/PTO 05 SEP 2000

PATENT
674537-2002

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s)	:	COIA et al.
U.S. Serial No.	:	Filed Concurrently Herewith
Int'l Appln. No.	:	PCT/AU99/00136
Int'l Filing Date	:	05 March 1999
Earliest Priority Date	:	06 March 1998
For	:	V-LIKE DOMAIN BINDING MOLECULES

745 Fifth Avenue
New York, NY 10151

EXPRESS MAIL

Mailing Label Number: EL588273756US

Date of Deposit: September 5, 2000

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(Signature of person mailing paper or fee)

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Box PCT
Washington, D.C. 20231

Dear Sir:

Preliminary to the examination of this U.S. national phase application, please enter the following amendments:

IN THE SPECIFICATION:

Page 1, below "V-like Domain Binding Molecules" please insert:

--RELATED APPLICATIONS

This application is the National Phase of PCT/AU99/00136, filed March 5, 1999, designating the U.S. and published as WO 99/45110, with a claim of priority from Australian application no. PP2210, filed March 6, 1998. All of the foregoing applications, as well as all documents cited in the foregoing applications ("application documents") and all documents cited or referenced in application documents are hereby incorporated herein by reference. Also, all documents cited in this application ("herein cited documents") and all documents cited or referenced in herein cited documents are hereby incorporated herein by reference.

IN THE CLAIMS:

Claim 7, line 1, please delete "any one of claims 1 to 6" and insert --claim 1--;

Claim 9, line 1, please delete "any one of claims 1 to 8" and insert --claim 1--;

Claim 10, line 1, please delete "any one of claims 1 to 9" and insert --claim 1--;

Claim 13, line 1, please delete "any one of claims 1 to 12" and insert --claim 1--;

Claim 15, line 1, please delete "any one of claims 1 to 12" and insert --claim 1--;

Claim 17, line 1, please delete "or claim 16";

Claim 18, line 1, please delete "any one of claims 1 to 17" and insert --claim 1--;

Claim 20, line 2, please delete "any one of claims 1 to 19" and insert --claim 1--;

Claim 21, lines 1-2, please delete "any one of claims 1 to 20" and insert --claim 1--;

Claim 22, line 2, please delete "any one of claims 1 to 20" and insert --claim 1--;

Claim 26, line 2, please delete "or claim 25";

Claim 28, line 2, please delete "any one of claims 1 to 20" and insert --claim 1--;

Claim 29, line 3, please delete "any one of claims 1 to 20" and insert --claim--.

IN THE ABSTRACT:

Please add the Abstract attached hereto as a separate sheet.

REMARKS

This application includes multiple claim dependencies. The amendment removes the multiple claim dependencies, and the filing fee for this application was computed on the basis that no dependent claim depends from more than one preceding claim. The amendment also adds headings and other formalities.

Entry of this amendment and an early examination on the merits are respectfully solicited.

Respectfully submitted,
FROMMER LAWRENCE & HAUG LLP

By: _____
Thomas J. Kowalski
Reg. No. 32,147
(212) 588-0800

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ABSTRACT

The present invention relates to novel binding moieties comprising at least one monomeric V-like domain (VLD) derived from a non-antibody ligand, the at least one monomeric V-like domain being characterized in that at least one CDR loop structure or part thereof is modified or replaced such that the solubility of the modified VLD is improved when compared with the unmodified VLD.

Docket No. 674537-2002

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V-like Domain Binding Molecules

Field of the Invention

The present invention relates to V-like Domain binding molecules with affinities for target molecules. The present invention also relates to compositions comprising these V-like domain binding molecules and to methods of diagnosis or treatment which involve the use of these molecules. The present invention also relates to a method for selecting V-like Domain binding molecules with novel binding affinities and/or specificities.

Background of the Invention

Immunoglobulin Superfamily - Antibody Variable (V) Domains

Antibodies are the paradigm of specific high-affinity binding reagents and provide an antigen binding site by interaction of variable heavy (V_H) and variable light (V_L) immunoglobulin domains. The binding interface is formed by six surface polypeptide loops, termed complementarity determining regions (CDRs), three from each variable domain, which are highly variable and combined provide a sufficiently large surface area for interaction with antigen. Specific binding reagents can be formed by association of only the V_H and V_L domains into an Fv module. Bacterial expression is enhanced by joining the V-domains with a linker polypeptide into a single-chain scFv molecule. "Humanisation" of recombinant antibodies by grafting murine CDR loop structures onto a human Fv framework is disclosed by Winter et al EP-239400.

Methods to improve the expression and folding characteristics of single-chain Fv molecules were described by Nieba et al (1997). The properties of single V-domains, derived from natural mammalian antibodies, have been described by Gussow et al in WO/90/05144 and EP 0368684B1 and by Davis et al in WO/91/08482. Single camelid V-domains have been described by Hamers et al in WO/96/34103 and in WO/94/25591. A method for reducing the hydrophobicity of the surface of a human V_H domain by replacing human amino acid sequences with camelid amino acid sequences was described by Davies and Riechmann (1994). Methods to exchange other regions of human V_H sequences with camel sequences to further enhance protein stability, including the insertion of cysteine residues in CDR loops, were described by Davies and Riechmann (1996).

Several attempts to engineer high-affinity single domain binding reagents using either the V_H or V_L domains alone have been unsuccessful, due to lack of binding specificity and the inherent insolubility of single domains in the absence of the hydrophobic face where the V_H and V_L domains interact (Kortt et al, 1995).

T-cell Receptor Variable (V) Domains

The T-cell receptor has two V-domains that combine into a structure similar to the Fv module of an antibody that results from combination of the VH and VL domains. Novotny et al (1991) described how the two V-domains of the T-cell receptor (termed alpha and beta) can be fused and expressed as a single chain polypeptide and, further, how to alter surface residues to reduce the hydrophobicity directly analogous to an antibody scFv. Other publications describe the expression characteristics of single-chain T-cell receptors comprising two V-alpha and V-beta domains (Wulfing and Pluckthun,1994; Ward, 1991).

Non-antibody ligands - CTLA-4 and CD28 V-like Domains

There are a class of non-antibody ligands which bind to specific binding partners which also comprise V-like domains. These V-like domains are distinguished from those of antibodies or T-cell receptors because they have no propensity to join together into Fv-type molecules. These non-antibody ligands provide an alternative framework for the development of novel binding moieties with high affinities for target molecules. Single domain V-like binding molecules derived from these non-antibody ligands which are soluble are therefore desirable. Examples of suitable non-antibody ligands are CTLA-4, CD28 and ICOS (Hutloff et al, 1999).

Cytotoxic T-lymphocyte associated antigen 4 (CTLA-4) and the homologous cell-surface proteins CD28 and ICOS, are involved in T-cell regulation during the immune response. CTLA-4 is a 44 kDa homodimer expressed primarily and transiently on the surface of activated T-cells, where it interacts with CD80 and CD86 surface antigens on antigen presenting cells to effect regulation of the immune response (Waterhouse et al.1996, van der Merwe et al. 1997). CD28 is a 44kDa homodimer expressed predominantly on T-cells and, like CTLA-4, interacts with CD80 and CD86 surface antigens on antigen presenting cells to effect regulation of the immune response (Linsley et al.1990). Current theory suggests that competition between CTLA-4 and CD28 for available ligands controls the level of immune response, for

example, gene deletion of CTLA-4 in knock-out mice results in a massive over-proliferation of activated T-cells (Waterhouse et al. 1995).

Each CTLA-4 monomeric subunit consists of an N-terminal extracellular domain, transmembrane region and C-terminal intracellular domain. The extracellular domain comprises an N-terminal V-like domain (VLD: of approximately 14 kDa predicted molecular weight by homology to the immunoglobulin superfamily) and a stalk of about 10 residues connecting the VLD to the transmembrane region. The VLD comprises surface loops corresponding to CDR-1, CDR-2 and CDR-3 of an antibody V-domain (Metzler 1997). Recent structural and mutational studies on CTLA-4 suggest that binding to CD80 and CD86 occurs via the VLD surface formed from A'GFCC' V-like beta-strands and also from the highly conserved MYPPPY sequence in the CDR3-like surface loop (Peach et al. 1994: Morton et al. 1996: Metzler et al. 1997). Dimerisation between CTLA-4 monomers occurs through a disulphide bond between cysteine residues (Cys^{120}) in the two stalks, which results in tethering of the two extracellular domains, but without any apparent direct association between V-like domains (Metzler et al. 1997). Dimerisation appears to contribute exclusively to increased avidity for the ligands.

<u>In vitro Expression of Soluble Forms of CTLA-4.</u>

Neither the extracellular domains nor V-like domains (VLDs) of human CTLA-4 molecule have been successfully expressed as soluble monomers in bacterial cells, presumably due to aggregation of the expressed proteins (Linsley et al, 1995). Expression of the extracellular N-terminal domain (Met^{1} to Asp^{124}, comprising Cys^{120}) in *E.coli* results in production of a dimeric 28 kDa MW protein, in which two CTLA-4 V-like domains are joined by a disulphide linkage at Cys^{120}. Truncation at Val^{114} removes these cysteines and was intended to enable expression of a 14 kDa VLD in soluble, monomeric form. However, the product aggregated and it was concluded that hydrophobic sites, which were normally masked by glycosylation, were now exposed and caused aggregation (Linsley et al, 1995).

There have been some reports of successful expression of monomeric, glycosylated CTLA-4 extracellular domains in eukaryotic expression systems (ie CHO cells and the yeast Pichia pastoris; Linsley et al. 1995; Metzler et al. 1997; Gerstmayer et al. 1997). Glycosylation in these eukaryotic expression

systems is presumed to occur at the two N-linked glycosylation sites in the VLD (Asn76 and Asn108). However, high yields have only been described for expression of a gene encoding a CTLA-4 VLD fused to Ig-CH2/CH3 domains which produces a dimeric recombinant protein with 2 CTLA-4 VLDs attached to an Fc subunit (WO 95/01994 and AU 16458/95). AU 60590/96 describes mutated forms of CTLA-4 VLDs with single amino acid replacements of the first tyrosine (Y) in the MYPPPY surface loop which retain and modifies the affinity for the natural CD80 and CD86 ligands. AU 60590/96 describes the preferred soluble form of CTLA-4 VLDs as a recombinant CTLA-4/Ig fusion protein expressed in eukaryotic cells and does not solve the aggregation problem in prokaryote expression systems. EP 0757099A2 describes the use of CTLA-4 mutant molecules, for example the effect of changes on ligand binding of mutations in the CDR3-like loop.

Summary of the Invention

The present inventors have now developed novel binding molecules derived from the V-like domains (VLDs) of non-antibody ligands such as CTLA-4, CD28 and ICOS. Replacement of CDR loop structures within the VLDs results unexpectedly in the production of monomeric, correctly folded molecules with altered binding specificities and improved solubility.

Accordingly, in a first aspect the present invention provides a binding moiety comprising at least one monomeric V-like domain (VLD) derived from a non-antibody ligand, the at least one monomeric V-like domain being characterised in that at least one CDR loop structure or part thereof is modified or replaced such that the solubility of the modified VLD is improved when compared with the unmodified VLD.

Within the context of the present invention, the modification or replacement may involve any change to one or more physical characteristics (such as size, shape, charge, hydrophobicity etc) of the at least one CDR loop structure. The modification or replacement may result in a reduction in the size of the at least one CDR loop structure. In a preferred embodiment, however, at least one CDR loop structure or part thereof is modified or replaced such that

(i) the size of the CDR loop structure is increased when compared with corresponding CDR loop structure in the unmodified VLD; and/or

(ii) the modification or replacement results in the formation of a disulphide bond within or between one or more of the CDR loop structures.

In a second aspect, the present invention provides a binding moiety comprising at least one monomeric V-like domain (VLD) derived from a non-antibody ligand, the at least one monomeric V-like domain being characterised in that at least one CDR loop structure or part thereof is modified or replaced such that

(i) the size of the CDR loop structure is altered when compared with corresponding CDR loop structure in the unmodified VLD; and/or

(ii) the modification or replacement results in the formation of a disulphide bond within or between one or more of the CDR loop structures.

In a preferred embodiment of the second aspect, the size of the CDR loop structure is increased by at least two, more preferably at least three, more preferably at least six and more preferably at least nine amino acid residues.

In a further preferred embodiment, the modified binding moiety of the first or second aspect of the present invention also exhibits an altered binding affinity or specificity when compared with the unmodified binding moiety. Preferably, the effect of replacing or modifying the CDR loop structure is to reduce or abolish the affinity of the VLD to one or more natural ligands of the unmodified VLD. Preferably, the effect of replacing or modifying the CDR loop structure is also to change the binding specificity of the VLD . Thus it is preferred that the modified VLD binds to a specific binding partner which is different to that of the unmodified VLD.

The phrase "V-like domain" or "VLD" is intended to refer to a domain which has similar structural features to the variable heavy (V_H) or variable light (V_L) antibody. These similar structural features include CDR loop structures. By "CDR loop structures" we mean surface polypeptide loop structures or regions like the complementarity determining regions in antibody V-domains.

The phrase "non-antibody ligand" is intended to refer to any ligand which binds to a specific binding partner and which is not an antibody or a T-cell receptor. Examples of suitable non-antibody ligands are T-cell surface proteins such as CTLA-4, CD28 and ICOS. It will be appreciated by those skilled in the art that other non-antibody ligands which may provide V-like domains suitable for the invention are other T-cell surface proteins such as

CD2. CD4, CD7 and CD16: B cell surface proteins such as CD19, CD79a, CD22, CD33, CD80 and CD86: adhesion molecules such as CD48, CD541CAM and CD58. These molecules, which are listed in Table 1, provide a non-exhaustive list of structures which may form the basis for the single domain binding molecules of the present invention.

The phrase "V-like domain derived from a non-antibody ligand" is intended to encompass chimeric V-like domains which comprise at least part of a V-like domain derived from a non-antibody ligand.

TABLE 1: NON-ANTIBODY LIGANDS

Molecule	Size	Structure
Tcell Surface Proteins		
CD2	45-58kDa	VC[1] domains
CD4	55kDa	V2C2
CD7	40kDa	V domain
CD16	50-65kDa	2x C domains
B cell Surface Proteins		
CD19	95kDa	2x C domains
CD79a	33kDa	
CD22	130-140kDa	1xV 6xC domains
CD33	67kDa	VC domain
CD80	60kDa	VC domain
CD86	60kDa	VC domain
Adhesion molecules		
CD48	45kDa	VC domain
CD54ICAM	85-110kDa	
CD58	55-70kDa	VC domain

1 V = variable Ig domain, C = constant domain

These molecules are discussed in (1) The Leucocyte Antigen Facts Book, 1993, Eds Barclay et al., Academic Press, London; and (2) CD Antigens 1996 (1997) Immunology Today 18, 100-101, the entire contents of which are incorporated herein by reference.

The "solubility" of modified binding moieties of the present invention correlates with the production of correctly folded, monomeric domains. The solubility of the modified VLDs may therefore be assesed by HPLC. For example, soluble (monomeric) VLDs will give rise to a single peak on the HPLC chromatograph, whereas insoluble (eg. multimeric and aggregated) VLDs will give rise to a plurality of peaks. A person skilled in the art will therefore be able to detect an increase in solubility of modified VLDs using routine HPLC techniques.

It will be appreciated that the binding moieties of the present invention may be coupled together, either chemically or genetically, to form multivalent or multifunctional reagents. For example, the addition of C-terminal tails, such as in the native CTLA-4 with Cys^{120}, will result in a dimer.

The binding moieties of the present invention may also be coupled to other molecules for various diagnostic formulations. For example, the VLDs may comprise a C-terminal polypeptide tail or may be coupled to streptavidin or biotin for multi-site *in vitro* assays. The VLDs may also be coupled to radioisotopes, dye markers or other imaging reagents for *in vivo* detection and/or localisation of cancers, blood clots, etc. The VLDs may also be immobilised by coupling onto insoluble devices and platforms for diagnostic and biosensor applications.

In a most preferred embodiment of the first aspect of the present invention, the V-like domain is derived from the extracellular domain of the CTLA-4 molecule or the CD28 molecule. In a further preferred embodiment one or more surface loops of the CTLA-4 V-like domain and preferably the CDR-1, CDR-2 or CDR-3 loop structures are replaced with a polypeptide which has a binding affinity for a target molecule of interest. Target molecules of interest comprise, but are not limited to, drugs, steroids, pesticides, antigens, growth factors, tumour markers, cell surface proteins or viral coat proteins. It will be appreciated that these VLDs may be polyspecific, having affinities directed by both their natural surfaces and modified polypeptide loops.

In a further preferred embodiment the effect of replacing or modifying the CTLA-4, CD28 and ICOS V-like domain surface loops is to abolish the natural affinity to CD80 and CD86.

In one preferred embodiment, one or more of the CDR loop structures of the VLD are replaced with one or more CDR loop structures derived from an antibody. The antibody may be derived from any species. In a preferred embodiment, the antibody is derived from a human, rat, mouse, camel, llama or shark. The antibody or antibodies may be selected from the camel antibody cAB-Lys3 and the human anti-melanoma antibody V86.

In a further preferred embodiment, one or more of the CDR loop structures are replaced with a binding determinant derived from a non-antibody polypeptide. For example, one or more of the CDR loop structures may be replaced with a polypeptide hormone, such as somatostatin which is a 14 residue intra-disulphide bonded polypeptide important in cancer cell recognition, or with a viral protein such as the human influenza virus haemagglutinin protein.

In a further preferred embodiment the V-like domain of the binding moiety comprises CDR loop structures homologous in character to CDR loop structures found in camelid or llama antibodies. For example, the CDR loop structures may contain one or more non-conventional substitutions (eg. hydrophobic to polar in nature). In another preferred embodiment, the CDR-1 and CDR-3 loop structures may adopt non-canonical conformations which are extremely heterologous in length. The V-like domain may also possess a disulphide linkage interconnecting the CDR-1 and CDR-3 loop structures (as found in some camel $V_{H}H$ antibodies) or the CDR-2 and CDR-3 loop structures (as found in some llama $V_{H}H$ antibodies).

In a third aspect the present invention provides a polynucleotide encoding a binding moiety of the first or second aspect of the present invention. The polynucleotide may be incorporated into a plasmid or expression vector.

In a fourth aspect the present invention provides a prokaryotic or eukaryotic host cell transformed with a polynucleotide according to the third aspect of the present invention.

In a fifth aspect the present invention provides a method of producing a binding moiety which comprises culturing a host cell according to the fourth aspect of the present invention under conditions enabling expression of the binding moiety and optionally recovering the binding moiety.

In a preferred embodiment of the present invention the binding moiety is produced by expression in a bacterial host. Preferably, the binding moiety is unglycosylated.

In a sixth aspect the present invention provides a pharmaceutical composition comprising a binding moiety of the first or second aspect of the present invention and a pharmaceutically acceptable carrier or diluent.

In a seventh aspect the present invention provides a method of treating a pathological condition in a subject, which method comprises administering to the subject a binding moiety according to the first or second aspect of the present invention.

For *in vivo* applications it is preferable that VLDs are homologous to the subject of treatment or diagnosis and that any possible xenoantigens are removed. Accordingly it is preferred that VLD molecules for use in clinical applications are substantially homologous to naturally occurring human immunoglobulin superfamily members.

In an eighth aspect the present invention provides a method of selecting a binding moiety with an affinity for a target molecule which comprises screening a library of polynucleotides for expression of a binding moiety with an affinity for the target molecule, the polynucleotides encoding VLDs derived from one or more non-antibody ligands, wherein the polynucleotides have been subjected to mutagenesis which results in a modification or replacement in at least one CDR loop structure in at least one VLD and wherein the solubility of the isolated modified VLD is improved when compared with the isolated unmodified VLD.

It will be appreciated by those skilled in the art that within the context of the eighth aspect of the present invention, any method of random or targetted mutagenesis may be used to introduce modifications into the V-like domains. In a preferred embodiment, the mutagenesis is targetted mutagenesis. Preferably, the targetted mutagenesis involves replacement of at least one sequence within at least one CDR loop structure using splice overlap PCR technology.

It will also be appreciated by those skilled in the art that the polynucleotide library may contain sequences which encode VLDs comprising CDR loop structures which are substantially identical to CDR loop structures found in naturally occurring immunoglobulins as well as

sequences which encode VLDs comprising non-naturally occurring CDR loop structures.

In a preferred embodiment of the eighth aspect of the present invention. the screening process involves displaying the modified V-like domains as gene III protein fusions on the surface of bacteriophage particles. The library may comprise bacteriophage vectors such as pHFA, fd-tet-dog or pFAB.5c containing the polynucleotides encoding the V-like domains.

In a further preferred embodiment of the eighth aspect, the screening process involves displaying the modified V-like domains in a ribosomal display selection system.

Throughout this specification, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element. integer or step, or group of elements, integers or steps, but not the exclusion of any other element, integer or step, or group of elements, integers or steps.

Brief Description of the Drawings

Figure 1: CTLA-4 VLD-Specific Oligonucletides.

Figure 2: Polynucleotide sequence of complete cDNA encoding human CTLA-4 and polypeptide sequence of the VLD of human CTLA-4.

Figure 3: Display of CTLA-4 VLD STMs as gene 3 fusions on the surface of phage or phagemid. CTLA-4 VLD STMs are depicted as black spheroids; gene 3 protein is depicted as white spheroids; FLAG polypeptide is depicted in grey; genes are marked in a similar colour code and are depicted in an oval phage(mid) vector.

Figure 4: Schematic representation of the somatostatin polypeptide. Somatostatin (somatotropin release-inhibiting factor SRIF) is a cyclic 14-amino acid polypeptide. The cyclic nature is provided by a disulphide linkage between the cysteine residues at positions 3 and 14. The four residues which constitute the tip of the loop (Phe-Trp-Lys-Thr) are implicated in binding to members of the somatostatin receptor family.

Figure 5: Size exclusion HPLC profiles of affinity purified CTLA-4 VLD and CTLA-4-Som3 STM. Recombinant human CTLA-4 proteins were expressed in E. coli host TG1 from vector pGC, purified from periplasmic extracts by anti-FLAG affinity chromatography and subjected to size exclusion chromatography on a calibrated Superose 12 HR column. The elution profiles of purified CTLA-4 VLD and CTLA-4-Som3 STM are overlayed in this graph. CTLA-4 VLD comprises tetramer (21.86 min), dimer (26.83) and monomer (29.35 min). CTLA-4-Som3 STM comprises dimer (26.34) and monomer (29.28). Traces represent absorbance at 214 nm and are given in arbitrary units.

Figure 6: Schematic diagram of CTLA-4 VLD loop replacements. Construct A (CTLA-4 VLD: S2) represents the wild-type CTLA-4 extracellular V-domain, spanning residues 1-115. Constructs B (CTLA-4-Som1: PP2) and C (CTLA-4-Som1-Cys120; PP5) both contain the 14 residue somatostain polypeptide in CDR1. PP5 also carries a C-terminal extension containing Cys120. Construct D (CTLA-4-Som3; PP8) contains the 14 residue somatostatin polypeptide in place of CDR3. In construct E (CTLA-4-HA2: XX4), CDR2 has been replaced with a haemagglutinin tag. In construct F (CTLA-4-Som1-Som3: VV3), both CDR1 and CDR3 have been replaced with the somatostain polypeptide. In construct G (CTLA-4-Som-HA2-Som3: ZZ3) CDR1 and CDR3 are replaced with the somatostatin polypeptide whilst CDR2 is replaced with a haemagglutinin tag. In construct H (CTLA-4-anti-lys:2V8), all three CDR loop structures have been replaced with the CDR loops from a camel anti-lysozyme $V_{H}H$ molecule. Construct I (CTLA-4-anti-mel: 3E4) represents CTLA-4 VLD in which all three CDRs have been replaced by the VH CDR loops from anti-melanoma antibody V86 (Cai And Garen, 1997). PelB, cleavable pectate lyase secretion sequence (22 aa); flag, dual flag tag (AAADYKDDDDKAADYKDDDDK).

Figure 7: HPLC profiles of purified recombinant human CTLA-4 STMs. Recombinant CTLA-4 VLDs were expressed in E. coli host TG1 from vector pGC, purified from periplasmic extracts by anti-FLAG affinity chromatography and subjected to size exclusion chromatography on a calibrated Superose 12 HR column. The elution profiles of the purified proteins are shown. Panel A, CTLA-4 DIMER (PP5); Panel B, CTLA-4R (S2);

Panel C, CTLA-4-HA2 (XX4): Panel D, CTLA-4-Som3 (PP8); Panel E, CTLA-4-Som1 (PP2); Panel F, CTLA-4-Som1-Som3 (VV3); Panel G, CTLA-4-Som-HA2-Som3 (ZZ3); Panel H, CTLA-4-anti-lys (2V8): Panel I, CTLA-4-anti-mel (3E4).). Traces represent absorbance at 214 nm and are given in arbitrary units.

Figure 8: Comparison by size exclusion FPLC analysis of affinity purified CTLA-4 constructs synthesised using bacterial expression vector pGC or pPOW. Recombinant human CTLA-4R or its loop variants were expressed in E. coli host TOP10F', purified from periplasmic extracts by anti-FLAG affinity chromatography and subjected to size exclusion chromatography on a calibrated Superose 12 HR column. The elution profiles of proteins expressed from vector pGC are shown on the left, whilst proteins expressed from vector pPOW are shown on the right. Panel A, wild-type CTLA-4 VLD (S2); B, CTLA-4-Som1(PP2); C, CTLA-4-Som3(PP8); D, CTLA-4-Anti-lys(2V8); E, CTLA-4-Som1-HA2-Som3(ZZ3).

Figure 9: Protein stability analysis. Stability of monomer preparations of CTLA-4 VLD and loop variant constructs was analysed by size exclusion fplc chromatography on a precalibrated superose 12 hr (Pharmacia) column following several cycles of freeze/thawing. Aliquots of each protein were tested immediately after peak purification and following two cycles of freeze/thawing. A, CTLA-4 VLD (S2); B, CTLA-4-Som1 (PP2); C, CTLA-4-Som3 (PP8); D, CTLA-4-anti-lys (2V8); E, CTLA-4-Som-HA2-Som3 (ZZ3).

Figure 10: Lysozyme binding characteristics of CTLA-4-anti-lys construct 2V8.

Figure 11: Screening of CTLA-4 VLD phagemid library on immobilised Sh bleomycin.

Figure 12: Screening of CTLA-4 VLD libraries in solution

Detailed Description of the Invention

The present invention relates to the design of novel soluble VLD binding molecules derived from the V-like domain of immunoglobulin

superfamily members, such as the human CTLA-4 molecule. The preferred binding molecules of the present invention provide the following advantages (i) use of a native human protein obviates the need for subsequent humanisation of the recombinant molecule, a step often required to protect against immune system response if used in human treatment; (ii) the domain is naturally monomeric as described above (incorporation of residue Cys120 in a C-terminal tail results in production of a dimeric molecule); and (iii) structural modifications have resulted in improved E.coli expression levels.

Prior to publication of the first CTLA-4 structure determination, available sequence data and mutational analyses of both this molecule and CD28 were analysed. This allowed modelling and prediction of the regions corresponding to antibody CDR1, 2 and 3 regions. It was hypothesised that such areas would be susceptible to mutation or substitution without substantial effect upon the molecular framework and hence would allow expression of a correctly folded molecule. The subsequently published structure (Metzler et al. 1997) showed these predictions to be accurate, despite the unexpected separation of CDR1 from the ligand-binding site, and the extensive bending of CDR3 to form a planar surface contiguous with the ligand binding face.

In an initial set of experiments the V-like domain of the human CTLA-4 molecule was modified by replacement of CDR loop structures with either of two defined polypeptides. The two polypeptides were human somatostatin (Som) and a portion of the human influenza virus haemagglutinin protein (HA-tag). Somatostatin (SRIF: somatotropin release-inhibiting factor) is a 14 residue polypeptide comprising a disulphide bond that forces the central 10 residues into a loop. Human somatostatin is biologically widespread within the body and mediates a number of diverse physiological functions such as regulation of growth hormone secretion etc (Reisne, 1995). Human somatostatin binds a number of specific receptors (there are at least five subtypes) which have differing tissue specificities and affinities (Schonbrunn et al. 1995). These aspects of binding and activation are as yet poorly understood, but one salient feature is the high density of somatostatin receptors present on a number of cancerous cell lines, for example cancers of the neuro-endocrine system and small lung cancers (Reubi 1997). Artificial analogues of somatostatin have been produced for

imaging of such tumours which are resistant to degradation compared with the highly labile somatostatin polypeptide.

The haemagglutinin epitope sequence consists of the 9 residues YPYDVPDYA. A commercially produced antibody is available which specifically recognises this sequence. The epitope tag can be detected when randomly or directionally incorporated within the structure of proteins (Canfield et al. 1996).

Replacement of one or more CDR loop structures in the CTLA-4 V-like domain with somatostatin or the HA-tag resulted in the production of soluble, monomeric, unglycosylated binding molecules using different bacterial expression systems. This surprising finding shows that V-like domains provide a basic framework for constructing soluble, single domain molecules, where the binding specificity of the molecule may be engineered by modification of the CDR loop structures.

The basic framework residues of the V-like domain may be modified in accordance with structural features present in camelid antibodies. The camel heavy chain immunoglobulins differ from "conventional" antibody structures by consisting of only a single VH domain (Hamers-Casterman et al. 1993). Several unique features allow these antibodies to overcome the dual problems of solubility and inability to present a sufficiently large antigen binding surface.

First, several non-conventional substitutions (predominantly hydrophobic to polar in nature) at exposed framework residues reduce the hydrophobic surface, while maintaining the internal beta-sheet framework structure (Desmyter et al. 1996). Further, within the three CDR loops several structural features compensate for the loss of antigen binding-surface usually provided by the VL domain. While the CDR2 loop does not differ extensively from other VH domains, the CDR-1 and -3 loops adopt non-canonical conformations which are extremely heterologous in length. For example, the H1 loop may contain anywhere between 2-8 residues compared to the usual five in Ig molecules. However, it is the CDR3 loop which exhibits greatest variation: in 17 camel antibody sequences reported, the length of this region varies between 7 and 21 residues (Muyldermans et al. 1994). Thirdly, many camelid VH domains possess a disulphide linkage interconnecting CDRs -1 and -3 in the case of camels and interconnecting CDRs -1 and -2 in the case of llamas (Vu et al. 1997). The function of this structural feature appears to

be maintenance of loop stability and providing a more contoured, as distinct from planar, loop conformation which both allows binding to pockets within the antigen and gives an increased surface area. However, not all camelid antibodies possess this disulphide bond suggesting that it is not an absolute structural requirement.

These foregoing features have enabled camelid V-domains to present as soluble molecules in vivo and with sufficiently high affinity to form an effective immune response against a wide variety of target antigens. In contrast, cell surface receptors of the Ig superfamily (such as CD4 and CD2) comprise V-like binding domains and appear to bind cognate receptors with surface features other than the CDR loops. These V-like domains bind to cognate receptors with very low affinity. Physiological signalling between two cells are mediated by the avidity of multi-point binding, when two cell surfaces connect and each contains multiple receptors. CD2 is a well-characterised example: binding to CD58 is mediated by a highly constrained set of minor electrostatic interactions generated by charged and polar residues located in the GFCC'C" face (not the antibody type CDR-1, CDR-2 or CDR-3 loops). This results in a low affinity but highly specific interaction (Bodian et al 1994).

The present invention also relates to a method for generating and selecting single VLD molecules with novel binding affinities for target molecules. This method involves the application of well known molecular evolution techniques to V-like domains derived from members of the immunoglobulin superfamily. The method may involve the production of phage or ribosomal display libraries for screening large numbers of mutated V-like domains.

Filamentous fd-bacteriophage genomes are engineered such that the phage display, on their surface, proteins such as the Ig-like proteins (scFv, Fabs) which are encoded by the DNA that is contained within the phage (Smith, 1985; Huse et al., 1989; McCafferty et al., 1990; Hoogenboom et al., 1991). Protein molecules can be displayed on the surface of Fd bacteriophage, covalently coupled to phage coat proteins encoded by gene III, or less commonly gene VIII. Insertion of antibody genes into the gene III coat protein gives expression of 3-5 recombinant protein molecules per phage, situated at the ends. In contrast, insertion of antibody genes into gene VIII has the potential to display about 2000 copies of the recombinant protein per

phage particle, however this is a multivalent system which could mask the affinity of a single displayed protein. Fd phagemid vectors are also used, since they can be easily switched from the display of functional Ig-like fragments on the surface of Fd-bacteriophage to secreting soluble Ig-like fragments in E. coli. Phage-displayed recombinant protein fusions with the N-terminus of the gene III coat protein are made possible by an amber codon strategically positioned between the two protein genes. In amber suppressor strains of E. coli, the resulting Ig domain-gene III fusions become anchored in the phage coat.

A selection process based on protein affinity can be applied to any high-affinity binding reagents such as antibodies, antigens, receptors and ligands (see, for example, Winter and Milstein, 1991, the entire contents of which are incorporated herein by reference). Thus the selection of the highest affinity binding protein displayed on bacteriophage is coupled to the recovery of the gene encoding that protein. Ig-displaying phage can be affinity selected by binding to cognate binding partners covalently coupled to beads or adsorbed to plastic surfaces in a manner similar to ELISA or solid phase radioimmunoassays. While almost any plastic surface will adsorb protein antigens, some commercial products are especially formulated for this purpose, such as Nunc Immunotubes.

Ribosomal display libraries involve polypeptides synthesised de novo in cell-free translation systems and displayed on the surface of ribosomes for selection purposes (Hanes and Pluckthun, 1997; He and Taussig, 1997). The "cell-free translation system" comprises ribosomes, soluble enzymes required for protein synthesis (usually from the same cell as the ribosomes), transfer RNAs, adenosine triphosphate, guanosine triphosphate, a ribonucleoside triphosphate regenerating system (such as phosphoenol pyruvate and pyruvate kinase), and the salts and buffer required to synthesize a protein encoded by an exogenous mRNA. The translation of polypeptides can be made to occur under conditions which maintain intact polysomes, i.e. where ribosomes, mRNA molecule and translated polypeptides are associated in a single complex. This effectively leads to "ribosome display" of the translated polypeptide.

For selection, the translated polypeptides, in association with the corresponding ribosome complex, are mixed with a target molecule which is bound to a matrix (e.g. Dynabeads). The target molecule may be any

compound of interest (or a portion thereof) such as a DNA molecule, a protein, a receptor, a cell surface molecule, a metabolite, an antibody, a hormone or a virus. The ribosomes displaying the translated polypeptides will bind the target molecule and these complexes can be selected and the mRNA re-amplified using RT-PCR.

Although there are several alternative approaches to modify binding molecules the general approach for all displayed proteins conforms to a pattern in which individual binding reagents are selected from display libraries by affinity to their cognate receptor. The genes encoding these reagents are modified by any one or combination of a number of *in vivo* and *in vitro* mutation strategies and constructed as a new gene pool for display and selection of the highest affinity binding molecules.

In order that the nature of the present invention may be more clearly understood preferred forms thereof will now be described with reference to the following examples.

Example 1

Gene Construction and Cloning

CTLA-4 STM (STM: soluble truncated mutants of CTLA-4, used herein to describe CTLA-4 chimaeric V-like domain proteins) gene construction and cloning was by standard and well-described techniques (Polymerase chain reaction with specifically designed oligonucleotide primers, splice overlap extension, restriction enzyme digests etc). A list of oligonucleotide primers used is given in Figure 1.

The wild-type STM construct was amplified from cloned human CTLA-4 DNA (Figure 2) (and could be similarly amplified from reverse transcribed human cDNA by a competent worker in the field) using the oligonucleotide primers #3553 and #4316, which incorporated SfiI and NotI restriction sites at the 5' and 3' ends respectively. These terminal primers were used in all further constructions except: (i) where #4851 or #5443 was used to incorporate an ApaL1 site at the 5' end; (ii) where #4486 was used to add a C-terminal tail including residue Cys120; (iii) where #5467 was used to incorporate an EcoR1 site at the 5' end; and (iv) where the specific set of extension primers were used for ribosomal display.

A splice overlap PCR strategy using combinations of the oligonucleotides primers listed in Figure 1 was used to produce variations of

CDR-1, CDR-2 and/or CDR-3 loop structure replacements. The variations, which are described in greater detail in the following examples are listed in Table 2.

TABLE 2

CDR-1 combinations

	CDR-1	
CTLA-4 VLD	S^{19}FVCEYA.**SPGKATE**.....	VRV...
Anti-lysozyme	S^{19}FVCEYA.**SGYTIGPYCMG**.....	VRV...
Somatostatin-14	S^{19}FVCEYA.**AGCKNFFWKTFTSCATE**.	VRV...
Anti-melanoma	S^{19}FVCEYA.**SGFTFSSYAMS**.....	VRV...
Randomisation 1	S^{19}FVCEYA.**XXXXXXXG**.....	VRV...
Randomisation 2	S^{19}FVCEYA.**XXXXXXXXCXG**.....	VRV...
Randomisation 3	S^{19}FVCEYA.**XXarXarXXarCXG**.....	VRV...
Randomisation 4	S^{19}FVCEYA.**SPGXXXX**.....	VRV...
Randomisation 5	S^{19}FVCEYA.**SPGXCXX**.....	VRV...
Randomisation 6	S^{19}FVCEYA.**XXXXXXXXATE**.....	VRV...
Randomisation 7	S^{19}FVCEYA.**XXXXXXCXATE**.....	VRV...
Randomisation 8	S^{19}FVCEYA.**AGCKNXXXXXXTSCATE**.	VRV...

CDR-2 combinations

	CDR-2
CTLA-4 VLD	Q^{44}VTEVCAA.**TYMMGNELTF**.LDDSICT...
Anti-lysozyme	Q^{44}VTEVCAA.**AINMGGGITF**.LDDSICT...
Haemagglutinin tag	Q^{44}VTEVCAA.**TYPYDVPDYA**.LDDSICT...
Anti-melanoma	Q^{44}VTEVCAA.**AISGSGGSTY**.LDDSICT...
Randomisation 1	Q^{44}VTEVCAA.**TYXXGXELTF**.LDDSICT...
Randomisation 2	Q^{44}VTEVCAA.**CYXXGXELTF**.LDDSICT...

CDR-3 combinations

		CDR-3	
	CTLA-4 VLD	C^{93}KV.**ELMYPPPYYL**.....	GIG...
	Anti-lysozyme	C^{93}KV.**DSTIYASYYEC**GHGLSTGGYGYDS.	GIG...
	Somatostatin-14	C^{93}KV.**EAGC**KNFFWKTFTSC.....	GIG...
	Anti-melanoma	C^{93}KV.**GWGLRGEEGDYYMDV**.....	GIG...
	Randomisation 1	C^{93}KV.**XXXXXXXXXXX**.....	GIG...
	Randomisation 2	C^{93}KV.**XXXXXXXXXXXXXXX**.....	GIG...
	Randomisation 3	C^{93}KV.**XXXXXX.C.XXXX**.....	GIG...
	Randomisation 4	C^{93}KV.**XXXXXXX.C.XXXX**.....	GIG...
	Randomisation 5	C^{93}KV.**XXXXXXXX.C.XXXXX**.....	GIG...
	Randomisation 6	C^{93}KV.**XXXXXXXXXX.C.XXXXXXX**.....	GIG...
	Randomisation 7	C^{93}KV.**EXXXXXXXXX**.....	GIG...
	Randomisation 8	C^{93}KV.**EXXXXXX.C.XXXXXXX**.....	GIG...
	Randomisation 9	C^{93}KV.**EAGCKNXXXXXXTSC**.....	GIG...

For generation of randomised sections of the CDR loop structures, similar splice-overlap techniques were used with oligonucleotides where a given triplet(s) were encoded by the sequence NNg/T where N represents any of the four possible nucleotide bases. This combination covers all possible amino acid residues. Alternatively, randomisation was biased towards certain subsets of amino acids (for example aromatic residues, Figure 1, #5452).

In some instances, a variant technique was used for STM gene construction, where randomised oligonucleotide primers were designed which incorporated restriction sites for direct cloning into the similarly modified (with complementary restriction sites) CTLA-4 VLD framework (for example Figure 1, #4254).

Completed constructs were cut with approriate combinations of restriction enzymes (for example Sfi1,Not1, ApaL1, EcoR1) and cloned into like sites in appropriate expression vectors. These vectors comprise: (i) for production of soluble protein expression vectors pGC (Coia et al, 1996) and pPOW (Power et al, 1992; Kortt et al. 1995) (ii) for bacteriophage and

phagemid display, completed STM constructs were cut with the restriction enzymes SfiI and NotI or ApaLI and NotI and cloned into the vectors pHFA, and pFAB.5c (phagemid) or pfd-Tet-DOG (phage). These vectors allow display of the STMs as gene3 protein fusions on the surface of bacteriophage in 1-2 (phagemid) or 3-5 (phage) copies per bacteriophage particle (Figure 3).

All DNA constructs were verified by restriction analysis and DNA sequencing and tested for expression of recombinant protein by standard and well-understood techniques (Polyacrylamide gel electrophoresis, Western blot etc).

Example 2

Production and Isolation of Recombinant STM Proteins

Recombinant proteins were produced using vectors which represent different protocols for periplasmic expression systems. These vectors were (i) pGC: this vector allows high level expression of heterologous proteins by chemical (IPTG) induction, which are targeted to the periplasmic space by means of a leader sequence. The leader sequence is subsequently cleaved to produce the mature protein. In addition, this vector contains two in-frame 8 residue tag sequences (FLAG tags) which allow affinity purification of the recombinant protein. (ii) pPOW, which, like pGC, allows high level heat inducible expression of proteins targeted to the periplasmic space by means of a cleavable leader sequence and two in-frame 8 residue tag sequences (FLAG tags).

Recombinant proteins were purified by the following methods, which are but two variations of well established techniques. (i) Bacterial clones in vector pGC were grown overnight in 2YT medium/37°C /200 rpm/100mg/ml ampicillin, 1% glucose (final). Bacteria were diluted 1/100 into either 0.5 or 2l of 2YT medium supplemented with 100mg/ml ampicillin, 0.1% glucose (final), and grown at 28°C/ 200 rpm. These cultures were grown to an optical density of between 0.2-0.4, at which stage they were induced with 1mM IPTG (final). Cultures were allowed to grow for 16 hours (overnight) before harvesting. Bacteria were collected by centrifugation (Beckman JA-14 rotor or equivalent/6K/10min/4°C) and the periplasmic fraction collected by standard techniques. Briefly, this involved resuspension of bacterial pellets in a 1/25th volume of spheroplast forming buffer consisting of 100mM Tris-HCl/0.5M sucrose/0.5 mM EDTA (pH8.0), followed by addition of 1/500th

volume of hen egg lysozyme (2mg/ml in water) and incubation for 10min. A 0.5x solution of the above spheroplasting buffer was then added to a final volume of 1/5th of the original culture, and the incubation continued for a further 20min. The cell debris was then pelleted by centrifugation (Beckman JA-14 rotor or equivalent/9K/15min/4°C) and the supernatant containing the periplasmic fraction collected. All of the above procedures were performed at 4°C. Samples were processed immediately by sonication, filtration through a 0.45μ nitrocellulose membrane and processed immediately or stored at 4°C in the presence of sodium azide (0.05%). If freezing was required, no more than one freeze-thaw cycle was allowed. (ii) Bacterial clones in pPOW were grown overnight at 30°C in 100 ml 2xYT broth containing 100 μg/ml (w/v) ampicillin. On the following day cultures were used to inoculate 900 ml fresh 2xYT broth containing 100 μg/ml (w/v) ampicillin, to OD600nm = 0.2-0.5, and grown at 30°C with shaking (150-200 rpm) until OD600nm = 4 i.e. late log phase. To induce recombinant protein expression, the temperature was raised to 42°C for 1 hour and then dropped to 20°C for a further hour. Cells were harvested by centrifugation (Beckman JA-14 /6K rpm/5 min/4°C), the cell pellet resuspended in 100 ml extraction buffer (20mM Tris pH 8.0/ 0.2mg/ml (w/v) lysozyme/0.1% (v/v) Tween-20) and incubated at 4°C overnight. Samples were sonicated for 30 seconds and cellular debris collected by centrifugation (Beckman JA-14 /14K rpm/10 min/4°C). The aqueous phase, containing the "lysozyme" wash, was retained. Cell pellets were then washed twice with ice-cold water and this "osmotic shock" wash was retained. Each wash consisted of resuspending the pellet in 100 ml ice-cold water followed by incubation on ice for 10 minutes in the first instance followed by 1 hour in the second instance. Following centrifugation (Beckman JA-14 /14K rpm/10 min/4°C), the pH of the aqueous phase was adjusted by addition of 10 ml 10xTBS, pH 8. The "lysozyme" and "osmotic shock" washes were pooled and constitute the soluble or "periplasmic" protein fraction. Periplasmic fractions were sonicated, filtered through a 0.45μ nitrocellulose membrane and processed immediately or stored at 4°C in the presence of sodium azide (0.05%), PMSF (23 μg/ml) and EDTA (50 mM).

Recombinant proteins were purified by affinity chromatography through a divinyl sulphone activated agarose (Mini-Leak)-linked anti-FLAG antibody column. Periplasmic extracts were directly loaded onto a 10 ml

anti-FLAG column which had been pre-equilibrated in TBS (pH 8) containing 0.05% (w/v) sodium azide. Bound proteins were eluted with Immunopure Gentle Ag/Ab Elution Buffer (Pierce). Samples were then dialysed against TBS/0.05% (w/v) azide (pH 8), concentrated by ultrafiltration over a 3 kDa cut-off membrane (YM3, Diaflo), and analysed by HPLC on a pre-calibrated Superose 12 HR or Superdex 200 HR column (Pharmacia Biotech), at a flow rate of 0.5 ml/min. Fractions corresponding to monomeric , dimeric and tetrameric species were collected, concentrated as above, and stored at 4°C prior to analysis. Protein concentration was determined spectrophotometrically using an extinction coefficient at A280 of 1.27 for the CTLA-4R extracellular domain, 0.92 for CTLA-4-Som1, 1.13 for CTLA-4-Som3, 1.05 for CTLA-4-Anti-Lys. All of the above protein chemistry methods are standard techniques within the field. Purified proteins were analysed by standard techniques for example polyacrylamide gel electrophoresis, western blot, dot blot etc.

Cloning and expression in the bacteriophage expression vectors pHFA, pFAB.5c and fd-tet dog, and subsequent production of recombinant bacteriophage, were by standard and well-established techniques. Screening of libraries of randomised CTLA-4 STMs was by standard and well-established techniques (Galanis et al 1997).

Example 3

CTLA-4 STMs incorporating Somatostatin and Haemagglutinin Peptides.

Initially the CDR1 or the CDR3 loop structures of the CTLA-4 STM were replaced with the somatostatin polypeptide. This 14 residue polypeptide is conformationally constrained by an intra-disulphide linkage between Cys3 and Cys14 (Figure 4). This was reasoned to form a discrete protein loop, analogous to the CDR loops found in antibodies, and particularly analogous to the long CDRs found in camelid antibodies which are also stabilised by a disulphide linkage. The effect of substituting CDR1 in the presence or absence of Cys120 ie. whether a dimer could be produced, was also tested. These experiments produced an unexpected and surprising result. Substitution of either CDR-1 or -3 with somatostatin significantly enhanced the production of monomeric protein. This is illustrated in Figure 5 where replacement of the CDR-3 loop structure with somatostatin

significantly increased the ratio of monomeric to dimeric/tetrameric protein species.

In further experiments, simultaneous replacement of both CDR-1 and -3 loop structures by somatostatin resulted in production of high-levels of monomeric protein. This shows that extensive loop structure replacements can be accommodated by the CTLA-4 scaffolding. Structurally, one of the somatostatin loops may lie flat against the face of the molecule in a manner analogous to that of the CDR-3 loop structure of CTLA-4 VLD.

In a further extension of the CDR loop structure-replacement strategy, a region corresponding to CDR-2 was replaced with the 8-residue haemagglutinin (HA) tag sequence. Use of the conformationally constrained somatostatin loop in this position was considered unsuitable as this region partially encompasses the C" beta strand running the length of the molecule. The HA tag could be detected upon this CTLA-4 STM by use of an anti-HA antibody. Gel filtration experiments showed the presence of a range of protein species, from monomeric through to aggregated species suggesting that CDR-2-only substitutions were not stable (Figures 6,7).

Final proof of principle that the CTLA-4 CDR loop structures could be replaced with other polypeptides to produce monomeric, soluble, STMs was by simultaneous replacement of all three CDR loop structures with two somatostatin and one HA epitope respectively. This STM produced a correctly folded and monomeric protein upon gel filtration chromatography (Figures 6,7).

The positions of CDR loop structure substitutions within the CTLA-4 VLD for the various STMs are shown in figure 6. HPLC profiles of affinity-purified STM proteins are shown in figure 7. Identical results were obtained for proteins produced in two different protein expression systems: pGC where protein expression is chemically induced, and pPOW where protein expression is temperature induced (see Example 2)(Figure 8). Polyacrylamide gel electrophoresis followed by western blot analysis indicated that the CTLA-4 STMs could be reduced and ran at the expected molecular weights and absent of glycosylation. Testing of isolated monomeric STM proteins showed that they remained monomeric after zero, one, or two freeze-thaw cycles (figure 9).

CTLA-4 STMs retained the correct conformation since a conformationally-specific anti-CTLA-4 antibody recognised STMs with both

CDR1 and -3 loop structure replacements. Interestingly, this antibody recognised the wild type monomer and the dimer (CDR1 replaced) poorly, contrasting with the strong reaction observed for the modified protein species. This suggests that in the wild type STM some form of local interaction is occurring that occludes the antibody binding site, and that this interaction is similar to the result when two CTLA-4 molecules are tethered together (presumably blocking access to the antibody).

Example 4

CTLA-4 STMs Based Upon a Camel anti-Lysozyme Antibody.

The camel V_HH antibody cAb-Lys3 isolated from immunised camels specifically binds within the active site cleft of hen egg lysozyme (Desmyter et al. 1996). To illustrate the ability of CTLA-4 STMs to function in a similar fashion, the three CDR loop structures of CTLA-4 VLD STM were replaced with the three CDR loop regions from cAb-Lys3. Positions and sequence of the substitutions are shown in figure 6. Expression of this STM (2V8) in either pGC or pPOW based expression systems resulted in production of predominantly monomeric soluble protein (Figures 7, 8). Protein solubility of this CTLA-4 STM was superior to native CTLA-4 VLD. ELISA analysis showed that (pGC produced) purified monomeric protein specifically bound hen egg lysozyme compared to non-specific antigens and compared to the CTLA-4 STM with somatostatin substituted within the CDR1 loop structure (PP2) (Figure 10A). Real-time binding analysis by BIAcore showed that the lysozyme specifically bound to immobilised anti-lysozyme STM (Figure 10B). The CTLA-4 STM framework is thus folding correctly and presenting the CDR loop structures in a manner in which they can bind lysozyme antigen. To further enhance expression of the CTLA-4 VLD anti-lysozyme, the coding sequence was adjusted by splice overlap PCR to comprise codons preferential for *E.coli* expression.

Example 5

CTLA-4 STMs Based Upon a Human anti-Melanoma Antibody.

The human-derived anti-melanoma antibody V86 specifically binds human melanoma cells. This antibody is unusual in that binding affinity resides entirely within the V_H region, addition of a cognate V_L decreases binding efficiency, and that the V_H domain expressed with a small segment

of the V_L domain has a high degree of solubility (Cai and Garen, 1997). To further illustrate that replacement of CTLA-4 VLD CDR loop structures enhances solubility and that the resultant STMs can be produced in bacterial expression systems, the three CDR loop structures of CTLA-4 were replaced with the three CDR loop regions from V86. Positions and sequence of the substitutions are shown in Figure 6. Expression of this STM (3E4) in pGC again resulted in production of predominantly monomeric soluble protein (Figure 7) with enhanced solubility compared to the CTLA-4 VLD.

Example 6

Construction of CTLA-4 STMs as Libraries of Binding Molecules

To select CTLA-4 STMs with novel binding specificities, VLD libraries were produced containing randomised CDR1 and CDR3 loop structures. Oligonucleotide primers used for library construction are listed in figure 1. Combinations of oligonucleotide primers used for library construction are shown in Table 3.

Table 3. CTLA-4 STM Library Combinations

CDR1

CDR3	4483*	4254	5449	5451	5452	5450	5446	4835
4482	+1	+1	//////////	//////////	//////////	//////////	//////////	//////////
4275	+1	+1	//////////	//////////	//////////	//////////	//////////	//////////
5470	//////////	//////////	+2	+2	+2	+2	+2	//////////
5474	//////////	//////////	+2	+2	+2	+2	+2	//////////
5471	//////////	//////////	+2	+2	+2	+2	+2	//////////
5472	//////////	//////////	+2	+2	+2	+2	+2	//////////
5475	//////////	//////////	+2	+2	+2	+2	+2	//////////
5473	//////////	//////////	+2	+2	+2	+2	+2	//////////
4836	//////////	//////////	//////////	//////////	//////////	//////////	//////////	+3

*: oligonucleotide number.

+ : library combination.

1,2,3: describes library number.

DNA constructs encoding the resultant libraries were cloned into vectors pHFA or pFAB.5c for production of fd-phagemid based libraries and into pfd-Tet-Dog for production of fd-phage based libraries (see examples 1 and 2). Library 1 was cloned into vector pHFA and consisted of 2.1×10^7 independent clones. Library 3 was cloned into vectors pHFA (5.7×10^5 independent clones) and pfd-Tet-Dog (2.2×10^4 independent clones). Library 2 was cloned into pFAB.5c (1.7×10^7 independent clones) and into pfd-Tet-Dog (1.6×10^5 independent clones). Numbers of independent clones were determined by counting gross numbers of transformed colonies constituting the library, followed by assaying for the presence and proportion of CTLA-4 STM-specific DNA.

For library 2, the variability of the full library was tested by sequencing of representative clones. These results are presented in Table 4. The expected heterogeneity of insert size and sequence was observed. A high proportion of UAG termination codons were observed, consistent with the oligonucleotide randomisation strategy. To prevent these codons causing premature termination of the CTLA-4 STM gene3 protein fusions, libraries were transferred into the *E.coli* strains Tg-1 and JM109, which suppress this termination codon by insertion of a glutamic acid residue. Cysteine residues were present in the high numbers expected from the desgn of the oligonucleotides.and were in positions capable of forming intra- and inter-CDR loop structure disulphide bonds.

Table 4 CDR1 and CDR3 Inserts from a Representative Series of Library 2 Clones

CLONE	CDR1	CDR3
3M-2	ND1	LPSSDTRAYS
3M-3	QESGGRPG	LPRGPPLLSL
3M-5	SPGRCLN	ND
3M-6	EWKR*HGG	LCPGACGCVY
3M-7	NSG*NEGG	ND
3M-11	DKPVTKSG	ND
3M-17	SPGACP*	ND
3M-18	SPGKCDQ	ND
3M-19	SPGMCAR	LMYPPPYYL
3M-20	ND	PFLFLPC*FFF
3N-1	WTLGHHKLCEG	LFTCLLALCS
3N-2	SPGECYG	SWLSTTXCLSSCS
3N-3	SPG*CQD	LLGSLLSCFASLS
3N-4	SPG*CQD	SPGSLLSCFASXS
3N-5	SPGRCTD	VICHSSVCLSD/EVC
3N-6	ND	DLPSYLACSI
3N-7	SPGRCDA	ALCWDVFYCSFPSY
3N-8	ELFGHARYCKG	VSITSP*LCPVKVFD
3N-9	SPGKV*N	LFVPFVSP
3N-12	SPGDLWV	ESGLSPVSPCSLYSL
3N-13	TSANGPYG	PWAYRFLAVL
3N-14	RKTREKYG	ELMYPPPYYLGI
3N-15	SPGQELT	ELFFLLYAPCYLFQR

ND: Not Done

*: UAG termination codon

Bacteriophage particles displaying CTLA-4 STMs as gene 3 protein fusions were rescued from *E.coli* cells by standard protocols and panned against antigens presented in a number of contexts as described in the following examples.

Example 7

CTLA-4 STM Libraries: Selection against Antigens on Solid Supports.

Four different antigens falling into a class of proteins with clefts or crevices within their structures were selected for screening. It was anticipated that the CTLA-4 VLD STMs, being of smaller size than antibodies, and possessing elongated CDR loop structures (especially CDR-3) would be able to access these cleft regions. The antigens selected were: (i) hen egg lysozyme (EC 3.2.1.17); (ii) bovine carbonic anhydrase (EC 4.2.1.1): (iii) fungal a-amylase (EC 3.2.1.1); and (iv) *Streptoalloteichus hindustanis* resistance protein ShBle (Gatignol et al. 1988). For binding to plates, antigens in coating buffer (1mg/ml in 0.1M NaHCO3 pH8.5) were bound to Costar ELISA plates by standard procedures. Rescued phage and phagemid-derived libraries were panned by standard and well-understood procedures except that lower than standard number of washes were employed to allow low affinity binding phage to be selected. Figure 11 shows titres of libraries selected against ShBle. After round 4, recovered bacteriophage titres were higher than controls. To those skilled in the art, this represents selection of specific binding moieties, and it is then a routine process to produce these selected CTLA-4 VLD STMs using expression vectors such as pGC or pPOW (as described in example 2).

Example 8

CTLA-4 STM Libraries: Selection against Antigens in Solution.

For selection in solution, the antigens bovine carbonic anhydrase and fungal a-amylase were biotinylated and selections performed in solution using capture by streptavidin coated magnetic beads. Throughout these experiments washes were kept constant at either 2 or 5 washes per selection round. Titres of recovered bacteriophage post-elution are shown in Figure 12. After round 4, recovered bacteriophage titres were higher than controls. To those skilled in the art, this represents selection of specific binding

moieties, and it is then a routine process to produce these selected CTLA-4 VLD STMs using expression vectors such as pGC or pPOW (as described in example 2).

Example 9

CTLA-4 STM Libraries: Selection in an Alternative Display and Selection System.

To allow further maturation and selection of antigen binding STMs, the CTLA-4 STM library was ligated into a plasmid to add a downstream C-terminal spacer polypeptide (heavy constant domain). Upstream transcriptional and translational initiation sequences were added by PCR amplification using specific oligonucleotides (Figure 1). This PCR DNA was used as a template for production of RNA followed by translation and display of the library on ribosomes in a coupled cell free translation system as described by He and Taussig (1997). To demonstrate binding, CTLA-4 STM ribosome complexes were panned on hepatitis B surface antigen (hbsa), glycophorin (glyA) and bovine serum albumin (BSA) coated dynabeads. RNA from ribosome complexes bound to hbsa, glyA and BSA was recovered by RT-PCR. It is then a routine process to clone these RT-PCR products into an expression vector such as pGC or pPOW (as described in example 2) allowing production of CTLA-4 STMs. It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention allowing display of libraries of CTLA-4 STMs as ribosome complexes (as in this example) as well as display on the surface of live cells (which may be derived from a eukaryotic or prokaryotic background) and may include bacteria, yeast, mammalian or insect cells.

Example 10

CTLA-4 STMs: Affinity Maturation and CDR2 Mutation.

To allow further maturation and selection of antigen-binding STMs, and the construction of randomised CDR-1, -2 and –3 libraries, CDR-2 randomised oligonucleotide primers were produced (Figure 1). A variation of these primers contained conserved cysteine residues to allow construction of STMs with CDR2-CDR3 disulphide linkages mimicing those found in llama single domain antibodies. Splice overlap PCR allowed creation of libraries containing all three CDR loop structures randomised.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

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Claims:

1. A binding moiety comprising at least one monomeric V-like domain (VLD) derived from a non-antibody ligand, the at least one monomeric V-like domain being characterised in that at least one CDR loop structure or part thereof is modified or replaced such that the solubility of the modified VLD is improved when compared with the unmodified VLD.

2. A binding moiety according to claim 1 in which at least one CDR loop structure or part thereof is modified or replaced such that

(i) the size of the CDR loop structure is increased when compared with the corresponding CDR loop structure in the unmodified VLD; and/or

(ii) the modification or replacement results in the formation of a disulphide bond within or between one or more of the CDR loop structures.

3. A binding moiety comprising at least one monomeric V-like domain (VLD) derived from a non-antibody ligand, the at least one monomeric V-like domain being characterised in that at least one CDR loop structure or part thereof is modified or replaced such that

(i) the size of the CDR loop structure is altered when compared with the corresponding CDR loop structure in the unmodified VLD; and/or

(ii) the modification or replacement results in the formation of a disulphide bond within or between one or more of the CDR loop structures.

4. A binding moiety according to claim 3 in which the size of the CDR loop structure is increased by at least two amino acid residues.

5. A binding moiety according to claim 3 in which the size of the CDR loop structure is increased by at least six amino acid residues.

6. A binding moiety according to claim 3 in which the size of the CDR loop structure is increased by at least nine amino acid residues.

7. A binding moiety according to any one of claims 1 to 6 in which the binding affinity of the modified VLD is altered when compared with the unmodified VLD.

8. A binding moiety according to claim 7 in which the affinity of the modified VLD to at least one natural ligand of the unmodified VLD is reduced.

9. A binding moiety according to any one of claims 1 to 8 in which the binding specificity of the modified VLD is different to that of the unmodified VLD.

10. A binding moiety according to any one of claims 1 to 9 in which the non-antibody ligand is a T-cell surface protein.

11. A binding moiety according to claim 10 in which the non-antibody ligand is CTLA-4, CD28 or ICOS.

12. A binding moiety according to claim 11 in which the non-antibody ligand is CTLA-4.

13. A binding moiety according to any one of claims 1 to 12 in which one or more of the CDR loop structures is replaced with a binding determinant derived from a non-antibody polypeptide.

14. A binding moiety according to claim 13 in which the binding determinant is derived from somatostatin or haemagglutinin.

15. A binding moiety according to any one of claims 1 to 12 in which one or more of the CDR loop structures is replaced with one or more CDR loop structures derived from an antibody or antibodies.

16. A binding moiety according to claim 15 in which the antibody or antibodies are derived from a rat, mouse, human, camel, llama or shark.

17. A binding moiety according to claim 15 or claim 16 in which the antibody or antibodies are selected from the camel antibody cAB-Lys3 and the human anti-melanoma antibody V86.

18. A binding moiety according to any one of claims 1 to 17 linked to a diagnostic reagent.

19. A binding moiety according to claim 18 in which the diagnostic reagent is selected from the group consisting of streptavidin, biotin , a radioisotope, dye marker or other imaging reagent.

20. A multivalent reagent comprising two or more binding moieties as claimed in any one of claims 1 to 19.

21. A binding moiety or multivalent reagent according to any one of claims 1 to 20 immobilised on a solid support or coupled to a biosensor surface.

22. A polynucleotide encoding a binding moiety or multivalent reagent as claimed in any one of claims 1 to 20.

23. A vector comprising a polynucleotide according to claim 22.

24. A host cell transformed with a vector as claimed in claim 23.

25. A host cell according to claim 24 in which the cell is a bacterial cell.

26. A method of producing a binding moiety which comprises culturing a host cell as claimed in claim 24 or claim 25 under conditions enabling expression of the binding moiety and optionally recovering the binding moiety.

27. A method according to claim 26 in which the binding moiety is unglycosylated.

28. A pharmaceutical composition comprising a binding moiety as claimed in any one of claims 1 to 20 and a pharmaceutically acceptable carrier or diluent.

29. A method of treating a pathological condition in a subject, which method comprises administering to the subject a binding moiety as claimed in any one of claims 1 to 20.

30. A method of selecting a binding moiety with an affinity for a target molecule which comprises screening a library of polynucleotides for expression of a binding moiety with an affinity for the target molecule, the polynucleotides encoding VLDs derived from one or more non-antibody ligands, wherein the polynucleotides have been subjected to mutagenesis which results in a modification or replacement in at least one CDR loop structure in at least one VLD and wherein the solubility of the isolated modified VLD is improved when compared with the isolated unmodified VLD.

31. A method according to claim 30 in which the screening process involves displaying the modified V-like domains as gene III protein fusions on the surface of bacteriophage particles.

32. A method according to claim 30 in which the screening process involves displaying the modified V-like domains in a ribosomal display selection system.

33. A binding moiety according to any one of claims 1 to 20 produced by a method according to any one of claims 30 to 32.

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SEQUENCE LISTING

Applicant: Diatech Pty Ltd

Title of Invention: V-like domain binding molecules

Prior Application Number: PP2210
Prior Application Filing Date: 1998-03-06

Number of SEQ ID NOs: 138

Software: PatentIn Ver. 2.1

SEQ ID NO: 1
Length: 6
Type: PRT
Organism: Homo sapiens

Sequence: 1
Met Tyr Pro Pro Pro Tyr
1 5

SEQ ID NO: 2
Length: 54
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 2
ttattactcg cggcccagcc ggccatggcc gcaatgcacg tggcccagcc tgct 54

SEQ ID NO: 3
Length: 60
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 3
ttattactcg cggcccagcc ggccatggcc gcaatgcacg tggcccagcc tgctgtggta 60

SEQ ID NO: 4
Length: 45
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 4
tctcacagtg cacaggcaat gcacgtggcc cagcctgctg tggta 45

SEQ ID NO: 5
Length: 39
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 5
tctcacagtg cacaggcaat gcacgtggcc cagcctgct 39

SEQ ID NO: 6
Length: 43
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 6
gcccagccgg ccgaattcgc aatgcacgtg gcccagcctg ctg 43

SEQ ID NO: 7
Length: 60
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 7
gcagctaata cgactcacta taggaacaga ccaccatgga cgtggcccag cctgctgtgg 60

SEQ ID NO: 8
Length: 42
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 8
atctgcggcc gctacataaa tctgggtacc gttgccgatg cc 42

SEQ ID NO: 9
Length: 66
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 9
gctgaattct gatcagtgat ggtgatggtg atgtgcggcc gcgtcagaat ctgggcacgg 60
ttctgg 66

SEQ ID NO: 10
Length: 51
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 10
gcccttgggc cgggagatgg tctgcttcag tggcgagggc aggtctgtgt g 51

SEQ ID NO: 11
Length: 49
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 11

cgagggcagg tctgtgtggg tcacggtgca cgtgaacctc tccccggag 49

SEQ ID NO: 12

Length: 51

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 12

cgtgaacctc tccccggagt tccagtcatc ctcgcagatg ctggcctcac c 51

SEQ ID NO: 13

Length: 84

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 13

agctttgtgt gtgagtatgc agctggctgc aagaatttct tctggaagac tttcacatcc 60

tgtgccactg aggtccgggt gaca 84

SEQ ID NO: 14

Length: 84

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 14

ctgggtaccg ttgccgatgc cacaggatgt gaaagtcttc cagaagaaat tcttgcagcc 60

agcctccacc ttgcagatgt agag 84

SEQ ID NO: 15

Length: 75

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 15

agctttgtgt gtgagtatgc agctggctgc aagaatnnkn nknnknnknn knnkacatcc 60

tgtgccactg aggtc 75

SEQ ID NO: 16

Length: 75

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 16

ctgggtaccg ttgccgatgc cacaggatgt mnnmnnmnnm nnmnnmnnat tcttgcagcc 60

agcctccacc ttgca 75

SEQ ID NO: 17

Length: 21

Type: DNA

Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 17
gtaggttgcc gcacagactt c 21

SEQ ID NO: 18
Length: 66
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 18
gaagtctgtg cggcaaccta cccgtatgac gttccggact acgccctaga tgattccatc 60
tgcacg 66

SEQ ID NO: 19
Length: 78
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 19
gccagctttg tgtgtgagta tgccagtggc tacaccatcg ggccgtactg catgggcgtc 60
cgggtgacag tgcttcgg 78

SEQ ID NO: 20
Length: 60
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 20
tgtgcggcag ccatcaacat gggcggtggc atcaccttcc tagatgattc catctgcacg 60

SEQ ID NO: 21
Length: 60
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 21
atctaggaag gtgatgccac cgcccatgtt gatggctgcc gcacagactt cagtcacctg 60

SEQ ID NO: 22
Length: 69
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 22

cagcccgtgg ccgcactcgt agtaggacgc gtagatcgtc gagtccacct tgcagatgta 60

gagtcccgt 69

SEQ ID NO: 23

Length: 72

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 23

aatctgggta ccgttgccga tgccggagtc atagccgtac cctcccgtgg acagcccgtg 60

gccgcactcg ta 72

SEQ ID NO: 24

Length: 78

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 24

gccagctttg tgtgtgagta tgccagtgga ttcaccttca gttcctacgc catgtccgtc 60

cgggtgacag tgcttcgg 78

SEQ ID NO: 25

Length: 51

Type: DNA

Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 25
gccatctccg gatccggagg ctcgacctac ctagatgatt ccatctgcac g 51

SEQ ID NO: 26
Length: 54
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 26
gtaggtcgag cctccggatc cggagatggc tgccgcacag acttcagtca cctg 54

SEQ ID NO: 27
Length: 69
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 27
cacgtccatg tagtagtctc cctcctcgcc gcgcagtccc cagcccacct tgcagatgta 60
gagtcccgt 69

SEQ ID NO: 28
Length: 51
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 28
aatctgggta ccgttgccga tgcccacgtc catgtagtag tctccctcct c 51

SEQ ID NO: 29
Length: 66
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 29
agctttgtgt gtgagtatgc annknnknnk nnknnknnkn nknnkgccac tgaggtccgg 60
gtgaca 66

SEQ ID NO: 30
Length: 68
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 30
cacgtggccc agcctgctgt ggtactggcc agcagccgag gcatcgccag ctttgtgtgt 60
gagtatgc 68

SEQ ID NO: 31
Length: 66
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 31
gtgtgtgagt acgcgtncnn snnsnnsnns nnsnnstgcn nsgctactga ggttcgtgtg 60
accgtc 66

SEQ ID NO: 32
Length: 73
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 32
gccagctttg tgtgtgagta tgcannknnk nnknnknnkn nknnkggcgt ccgggtgaca 60
gtgcttcggc agg 73

SEQ ID NO: 33
Length: 82
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR Primer

Sequence: 33

gccagctttg tgtgtgagta tgcannknnk nnknnknnkn nknnknnktg cnnkggcgtc 60

cgggtgacag tgcttcggca gg 82

SEQ ID NO: 34

Length: 82

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR Primer

Sequence: 34

gccagctttg tgtgtgagta tgcannknnk ywynnkywyn nknnkywytg cnnkggcgtc 60

cgggtgacag tgcttcggca gg 82

SEQ ID NO: 35

Length: 70

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 35

gccagctttg tgtgtgagta tgcatctcca ggcnnknnkn nknnkgtccg ggtgacagtg 60

cttcggcagg 70

SEQ ID NO: 36

Length: 70

Type: DNA

Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 36
gccagctttg tgtgtgagta tgcatctcca ggcnnktgcn nknnkgtccg ggtgacagtg 60
cttcggcagg 70

SEQ ID NO: 37
Length: 68
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 37
gtgactgaag tctgtgcggc aacctacnnk nnkgggnnkg agttgacctt cctagatgat 60
tccatctg 68

SEQ ID NO: 38
Length: 30
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 38
gtaggttgcc gcacagactt cagtcacctg 30

SEQ ID NO: 39
Length: 68
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 39
gtgactgaag tctgtgcggc atgctacnnk nnkgggnnkg agttgacctt cctagatgat 60
tccatctg 68

SEQ ID NO: 40
Length: 30
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 40
gtagcatgcc gcacagactt cagtcacctg 30

SEQ ID NO: 41
Length: 69
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 41

ctgggtaccg ttgccgatgc cmnnmnnmnn mnnmnnmnnm nnmnnmnnct ccaccttgca 60
gatgtagag 69

SEQ ID NO: 42

Length: 67

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 42

aggtggaann snnsnnsnns nnsnnstgcn nsnnsnnsnn snnsnnsnns ggcatcggca 60
acggtac 67

SEQ ID NO: 43

Length: 78

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 43

aatctgggta ccgttgccga tgccmnnmnn mnnmnnmnnm nnmnnmnnmn nmnncacctt 60
gcagatgtag agtcccgt 78

SEQ ID NO: 44

Length: 93

Type: DNA

Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 44
aatctgggta ccgttgccga tgcccagmnn mnnmnnmnnm nnmnnmnnmn nmnnmnnmnn 60
mnnmnnctcc accttgcaga tgtagagtcc cgt 93

SEQ ID NO: 45
Length: 81
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 45
aatctgggta ccgttgccga tgccmnnmnn mnnmnngcam nnmnnmnnmn nmnnmnncac 60
cttgcagatg tagagtcccg t 81

SEQ ID NO: 46
Length: 87
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 46
aatctgggta ccgttgccga tgccmnnmnn mnnmnnmnng camnnmnnmn nmnnmnnmnn 60
mnncaccttg cagatgtaga gtcccgt 87

SEQ ID NO: 47
Length: 99
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 47
aatctgggta ccgttgccga tgccmnnmnn mnnmnnmnnm nngcamnnmn nmnnmnnmnn 60
mnnmnnmnnm nnmnncacct tgcagatgta gagtcccgt 99

SEQ ID NO: 48
Length: 87
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 48
aatctgggta ccgttgccga tgccrwrmnn mnnmnnmnng camnnmnnmn nmnnmnnmnn 60
mnncaccttg cagatgtaga gtcccgt 87

SEQ ID NO: 49
Length: 70
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 49

atgcacgtgg cccagcctgc tgtggtgctg gccagcagcc gtggcatcgc cagctttgtg 60

tgtgaatatg 70

SEQ ID NO: 50

Length: 77

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:

Oligonucleotide PCR primer

Sequence: 50

gccagctttg tgtgtgaata tgcgtctggc tataccatcg gcccgtactg catgggtgtg 60

cgtgtgaccg tgctgcg 77

SEQ ID NO: 51

Length: 54

Type: DNA

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:

Oligonucleotide PCR primer

Sequence: 51

gtgcgtgtga ccgtgctgcg tcaggcggat agccaggtga ccgaagtttg cgcg 54

SEQ ID NO: 52

Length: 75

Type: DNA

Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 52
caggtgaccg aagtttgcgc ggcagcgatc aacatgggcg gtggcatcac cttcctggat 60
gattccatct gcacc 75

SEQ ID NO: 53
Length: 66
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 53
cagaccctgg atggtcaggt tcacctggtt accgctggag gtgccggtgc agatggaatc 60
atccag 66

SEQ ID NO: 54
Length: 57
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 54
cactttgcag atgtacagac cggtatccat ggcacgcaga ccctggatgg tcaggtt 57

SEQ ID NO: 55
Length: 66
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 55
caggccatga ccgcattcgt aataagacgc atagatggtg ctatccactt tgcagatgta 60
cagacc 66

SEQ ID NO: 56
Length: 69
Type: DNA
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:
Oligonucleotide PCR primer

Sequence: 56
ctgggtaccg ttgccgatgc cagaatcgta gccatagcca ccggtggaca ggccatgacc 60
gcattcgta 69

SEQ ID NO: 57
Length: 672
Type: DNA
Organism: Homo sapiens

Sequence: 57
atggcttgcc ttggatttca gcggcacaag gctcagctga acctggctgc caggacctgg 60
ccctgcactc tcctgttttt tcttctcttc atccctgtct tctgcaaagc aatgcacgtg 120
gcccagcctg ctgtggtact ggccagcagc cgaggcatcg ccagctttgt gtgtgagtat 180

gcatctccag gcaaagccac tgaggtccgg gtgacagtgc ttcggcaggc tgacagccag 240
gtgactgaag tctgtgcggc aacctacatg acggggaatg agttgacctt cctagatgat 300
tccatctgca cgggcacctc cagtggaaat caagtgaacc tcactatcca aggactgagg 360
gccatggaca cgggactcta catctgcaag gtggagctca tgtacccacc gccatactac 420
ctgggcatag gcaacggaac ccagatttat gtaattgatc cagaaccgtg cccagattct 480
gacttcctcc tctggatcct tgcagcagtt agttcggggt tgtttttta tagctttctc 540
ctcacagctg tttctttgag caaaatgcta aagaaaagaa gccctcttac aacaggggtc 600
tatgtgaaaa tgcccccaac agagccagaa tgtgaaaagc aatttcagcc ttattttatt 660
cccatcaatt ga 672

SEQ ID NO: 58
Length: 115
Type: PRT
Organism: Homo sapiens

Sequence: 58

Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly
1 5 10 15

Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
20 25 30

Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
35 40 45

Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp
50 55 60

Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
65 70 75 80

Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
85 90 95

Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Ala Gln
100 105 110

Ile Tyr Val
115

SEQ ID NO: 59
Length: 7
Type: PRT
Organism: Homo sapiens

Sequence: 59
Ser Pro Gly Lys Ala Thr Glu
1 5

SEQ ID NO: 60
Length: 9
Type: PRT
Organism: Homo sapiens

Sequence: 60
Tyr Met Met Gly Asn Glu Leu Thr Phe
1 5

SEQ ID NO: 61
Length: 9
Type: PRT
Organism: Homo sapiens

Sequence: 61
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu
1 5

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SEQ ID NO: 62
Length: 14
Type: PRT
Organism: Homo sapiens

Sequence: 62
Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
1 5 10

SEQ ID NO: 63
Length: 9
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Haemagglutinin tag

Sequence: 63
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

SEQ ID NO: 64
Length: 11
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Sequence from anti-lysozyme antibody

Sequence: 64
Ser Gly Tyr Thr Ile Gly Pro Tyr Cys Met Gly
1 5 10

SEQ ID NO: 65
Length: 10
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Sequence from anti-lysozyme antibody

Sequence: 65
Thr Tyr Met Met Gly Asn Glu Leu Thr Phe
1 5 10

SEQ ID NO: 66
Length: 24
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Sequence from anti-lysozyme antibody

Sequence: 66
Asp Ser Thr Ile Tyr Ala Ser Tyr Tyr Glu Cys Gly His Gly Leu Ser
1 5 10 15

Thr Gly Gly Tyr Gly Tyr Asp Ser
20

SEQ ID NO: 67
Length: 11
Type: PRT
Organism: Homo sapiens

Sequence: 67

Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5 10

SEQ ID NO: 68

Length: 10

Type: PRT

Organism: Homo sapiens

Sequence: 68

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
1 5 10

SEQ ID NO: 69

Length: 15

Type: PRT

Organism: Homo sapiens

Sequence: 69

Gly Trp Gly Leu Arg Gly Glu Glu Gly Asp Tyr Tyr Met Asp Val
1 5 10 15

SEQ ID NO: 70

Length: 21

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence: Flag-tag

Sequence: 70

Ala Ala Ala Asp Tyr Lys Asp Asp Asp Asp Lys Ala Ala Asp Tyr Lys
1 5 10 15

Asp Asp Asp Asp Lys
20

SEQ ID NO: 71
Length: 14
Type: PRT
Organism: Homo sapiens

Sequence: 71

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
1 5 10

SEQ ID NO: 72
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein

Sequence: 72

Ser Phe Val Cys Glu Tyr Ala Ser Gly Tyr Thr Ile Gly Pro Tyr Cys
1 5 10 15

Met Gly

SEQ ID NO: 73
Length: 24
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein

Sequence: 73
Ser Phe Val Cys Glu Tyr Ala Ala Gly Cys Lys Asn Phe Phe Trp Lys
1 5 10 15

Thr Phe Thr Ser Cys Ala Thr Glu
20

SEQ ID NO: 74
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein

Sequence: 74
Ser Phe Val Cys Glu Tyr Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala
1 5 10 15

Met Ser

SEQ ID NO: 75
Length: 15
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein containing random sequence

Sequence: 75
Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly
1 5 10 15

SEQ ID NO: 76
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein containing random sequence

Sequence: 76
Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1 5 10 15

Xaa Gly

SEQ ID NO: 77
Length: 21
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein containing random sequence

Sequence: 77

Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Ala Arg Xaa Ala Arg Xaa Xaa
1 5 10 15

Ala Arg Cys Xaa Gly
20

SEQ ID NO: 78

Length: 14

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:Fusion protein containing random sequence

Sequence: 78

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Xaa Xaa Xaa Xaa
1 5 10

SEQ ID NO: 79

Length: 14

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence:Fusion protein containing random sequence

Sequence: 79

Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Xaa Cys Xaa Xaa
1 5 10

SEQ ID NO: 80
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein containing random sequence

Sequence: 80
Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala
1 5 10 15

Thr Glu

SEQ ID NO: 81
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein containing random sequence

Sequence: 81
Ser Phe Val Cys Glu Tyr Ala Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Ala
1 5 10 15

Thr Glu

SEQ ID NO: 82
Length: 24
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence:Fusion protein containing random sequence

Sequence: 82
Ser Phe Val Cys Glu Tyr Ala Ala Gly Cys Lys Asn Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Thr Ser Cys Ala Thr Glu
20

SEQ ID NO: 83
Length: 25
Type: PRT
Organism: Homo sapiens

Sequence: 83
Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu
1 5 10 15

Thr Phe Leu Asp Asp Ser Ile Cys Thr
20 25

SEQ ID NO: 84
Length: 25
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein

Sequence: 84
Gln Val Thr Glu Val Cys Ala Ala Ala Ile Asn Met Gly Gly Gly Ile
1 5 10 15

Thr Phe Leu Asp Asp Ser Ile Cys Thr
20 25

SEQ ID NO: 85
Length: 25
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein

Sequence: 85
Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Pro Tyr Asp Val Pro Asp
1 5 10 15

Tyr Ala Leu Asp Asp Ser Ile Cys Thr
20 25

SEQ ID NO: 86
Length: 25
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein

Sequence: 86

Gln Val Thr Glu Val Cys Ala Ala Ala Ile Ser Gly Ser Gly Gly Ser
1 5 10 15

Thr Tyr Leu Asp Asp Ser Ile Cys Thr
20 25

SEQ ID NO: 87

Length: 25

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 87

Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Xaa Xaa Gly Xaa Glu Leu
1 5 10 15

Thr Phe Leu Asp Asp Ser Ile Cys Thr
20 25

SEQ ID NO: 88

Length: 25

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence: Fusion protein containing random sequence

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Sequence: 88

Gln Val Thr Glu Val Cys Ala Ala Cys Tyr Xaa Xaa Gly Xaa Glu Leu
1 5 10 15

Thr Phe Leu Asp Asp Ser Ile Cys Thr
20 25

SEQ ID NO: 89

Length: 13

Type: PRT

Organism: Homo sapiens

Sequence: 89

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu
1 5 10

SEQ ID NO: 90

Length: 27

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence: Fusion protein

Sequence: 90

Cys Lys Val Asp Ser Thr Ile Tyr Ala Ser Tyr Tyr Glu Cys Gly His
1 5 10 15

Gly Leu Ser Thr Gly Gly Tyr Gly Tyr Asp Ser
20 25

SEQ ID NO: 91
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein

Sequence: 91
Cys Lys Val Glu Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr
1 5 10 15

Ser Cys

SEQ ID NO: 92
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein

Sequence: 92
Cys Lys Val Gly Trp Gly Leu Arg Gly Glu Glu Gly Asp Tyr Tyr Met
1 5 10 15

Asp Val

SEQ ID NO: 93
Length: 14
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 93
Cys Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

SEQ ID NO: 94
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 94
Cys Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa

SEQ ID NO: 95
Length: 14
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 95

Cys Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1 5 10

SEQ ID NO: 96

Length: 15

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 96

Cys Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

SEQ ID NO: 97

Length: 17

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 97

Cys Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15

Xaa

SEQ ID NO: 98
Length: 21
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 98
Cys Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa
20

SEQ ID NO: 99
Length: 13
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 99
Cys Lys Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

SEQ ID NO: 100
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 100
Cys Lys Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa

SEQ ID NO: 101
Length: 18
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: Fusion protein containing random sequence

Sequence: 101
Cys Lys Val Glu Ala Gly Cys Lys Asn Xaa Xaa Xaa Xaa Xaa Xaa Thr
1 5 10 15

Ser Cys

SEQ ID NO: 102
Length: 10
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 102
Leu Pro Ser Ser Asp Thr Arg Ala Tyr Ser
1 5 10

SEQ ID NO: 103
Length: 8
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 103
Gln Glu Ser Gly Gly Arg Pro Gly
1 5

SEQ ID NO: 104
Length: 10
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 104
Leu Pro Arg Gly Pro Pro Leu Leu Ser Leu
1 5 10

SEQ ID NO: 105
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 105
Ser Pro Gly Arg Cys Leu Asn
1 5

SEQ ID NO: 106
Length: 8
Type: PRT
Organism: Artificial Sequence

Feature:
Name/Key: MOD_RES
Location: (5)
Other information: Stop codon but Glu when expressed in Tg-1 or JM109 strains of E.coli

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 106
Glu Trp Lys Arg Glu His Gly Gly
1 5

SEQ ID NO: 107
Length: 10
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 107
Leu Cys Pro Gly Ala Cys Gly Cys Val Tyr
1 5 10

SEQ ID NO: 108
Length: 8
Type: PRT
Organism: Artificial Sequence

Feature:
Name/Key: MOD_RES
Location: (4)
Other information: Stop codon but Glu when expressed in Tg-1 of JM109 E.coli strains

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 108
Asn Ser Gly Glu Asn Glu Gly Gly
1 5

SEQ ID NO: 109

Length: 8

Type: PRT

Organism: Artificial Sequence

Feature:

Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 109

Asp Lys Pro Val Thr Lys Ser Gly
1 5

SEQ ID NO: 110

Length: 7

Type: PRT

Organism: Artificial Sequence

Feature:

Name/Key: MOD_RES

Location: (7)

Other information: Stop codon but Glu when expressed in Tg-1 or JM109 strains of E. coli

Feature:

Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 110

Ser Pro Gly Ala Cys Pro Glu
1 5

SEQ ID NO: 111
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 111
Ser Pro Gly Lys Cys Asp Gln
1 5

SEQ ID NO: 112
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 112
Ser Pro Gly Met Cys Ala Arg
1 5

SEQ ID NO: 113
Length: 11
Type: PRT
Organism: Artificial Sequence

Feature:
Name/Key: MOD_RES
Location: (8)
Other information: Stop codon but Glu when expressed in Tg-1 or JM109 strains of E. coli

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 113
Pro Phe Leu Phe Leu Pro Cys Glu Phe Phe Phe
1 5 10

SEQ ID NO: 114
Length: 11
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 114
Trp Thr Leu Gly His His Lys Leu Cys Glu Gly
1 5 10

SEQ ID NO: 115
Length: 10
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 115
Leu Phe Thr Cys Leu Leu Ala Leu Cys Ser
1 5 10

SEQ ID NO: 116
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 116
Ser Pro Gly Glu Cys Tyr Gly
1 5

SEQ ID NO: 117
Length: 13
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 117
Ser Trp Leu Ser Thr Thr Xaa Cys Leu Ser Ser Cys Ser
1 5 10

SEQ ID NO: 118
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Name/Key: MOD_RES
Location: (4)
Other information: Stop codon but Glu when expressed in Tg-1 or JM109 strains of E. coli

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 118
Ser Pro Gly Glu Cys Gln Asp
1 5

SEQ ID NO: 119
Length: 13
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 119
Leu Leu Gly Ser Leu Leu Ser Cys Phe Ala Ser Leu Ser
1 5 10

SEQ ID NO: 120
Length: 13
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 120
Ser Pro Gly Ser Leu Leu Ser Cys Phe Ala Ser Xaa Ser
1 5 10

SEQ ID NO: 121
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 121
Ser Pro Gly Arg Cys Thr Asp
1 5

SEQ ID NO: 122
Length: 13
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 122
Val Ile Cys His Ser Ser Val Cys Leu Ser Asp Val Cys
1 5 10

SEQ ID NO: 123
Length: 13
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 123
Val Ile Cys His Ser Ser Val Cys Leu Ser Glu Val Cys
1 5 10

SEQ ID NO: 124
Length: 10
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 124
Asp Leu Pro Ser Tyr Leu Ala Cys Ser Ile
1 5 10

SEQ ID NO: 125
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 125
Ser Pro Gly Arg Cys Asp Ala
1 5

SEQ ID NO: 126
Length: 14
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 126
Ala Leu Cys Trp Asp Val Phe Tyr Cys Ser Phe Pro Ser Tyr
1 5 10

SEQ ID NO: 127
Length: 11
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 127
Glu Leu Phe Gly His Ala Arg Tyr Cys Lys Gly
1 5 10

SEQ ID NO: 128
Length: 15
Type: PRT
Organism: Artificial Sequence

Feature:
Name/Key: MOD_RES
Location: (7)
Other information: Stop codon but Glu when expressed in Tg-1 of JM019 strains of E. coli

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 128
Val Ser Ile Thr Ser Pro Glu Leu Cys Pro Val Lys Val Phe Asp
1 5 10 15

SEQ ID NO: 129
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Name/Key: MOD_RES
Location: (6)
Other information: Stop codon but Glu when expressed in Tg-1 or JM109 strains of E. coli

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 129
Ser Pro Gly Lys Val Glu Asn
1 5

SEQ ID NO: 130
Length: 8
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 130
Leu Phe Val Pro Phe Val Ser Pro
1 5

SEQ ID NO: 131
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 131
Ser Pro Gly Asp Leu Trp Val
1 5

SEQ ID NO: 132
Length: 15
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 132
Glu Ser Gly Leu Ser Pro Val Ser Pro Cys Ser Leu Tyr Ser Leu
1 5 10 15

SEQ ID NO: 133
Length: 8
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 133
Thr Ser Ala Asn Gly Pro Tyr Gly
1 5

SEQ ID NO: 134
Length: 10
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 134
Pro Trp Ala Tyr Arg Phe Leu Ala Val Leu
1 5 10

SEQ ID NO: 135
Length: 8
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 135
Arg Lys Thr Arg Glu Lys Tyr Gly
1 5

SEQ ID NO: 136
Length: 12
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 136
Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile
1 5 10

SEQ ID NO: 137
Length: 7
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 137
Ser Pro Gly Gln Glu Leu Thr
1 5

SEQ ID NO: 138
Length: 15
Type: PRT
Organism: Artificial Sequence

Feature:
Other information: Description of Artificial Sequence: CDR1 and CDR3 inserts possessing randomly generated sequence

Sequence: 138
Glu Leu Phe Phe Leu Leu Tyr Ala Pro Cys Tyr Leu Phe Gln Arg
1 5 10 15

FIGURE 1: CTLA-4 VLD-SPECIFIC OLIGONUCLEOTIDES

OLIGONUCLEOTIDE	NUMBER	SIZE	SEQUENCE[1]	FEATURES
For 5' CTLA-4 amplification	3553 5023 5671	54	TTATTACTCgCggCCCAgCCggCCATggCCgCAATgCACgTggCCCAgCCTgCT	forward primer + SfiI site
For 5' CTLA-4 amplification	5445	60	TTATTACTCgCggCCCAgCCggCCATggCCgCAATgCACgTggCCCAgCCTgCTgTggTA	forward primer + SfiI site
For 5' CTLA-4 amplification	5443	45	TCTCACAgTgCACAggCAATgCACgTggCCCAgCCTgCTgTggTA	forward primer + ApaLI site
For 5' CTLA-4 amplification	4851	39	TCTCACAgTgCACAggCAATgCACgTggCCCAgCCTgCT	forward primer + ApaLI site
For 5' CTLA-4 amplification	5467	43	gCCCAgCCggCCgAATTCgCAATgCACgTggCCCAgCCTgCTg	forward primer + EcoRI site
For 5' CTLA-4 amplification		60	GCAGCTAATACGACTCACTATAGGAACAGACCACCATGGACGTGGCCCAGCCTGCTGTGG	ribosomal display
//////////////////////////////////////	//////////	//////	//	//
For 3' CTLA-4 amplification	4316 5022 5670	42	ATCTgCggCCgCTACATAAATCTgggTACCgTTgCCgATgCC	reverse primer + NotI site
For 3' CTLA-4 amplification	4486	66	gCTgAATTCTgATCAgTgATggTgATggTgATgTgCggCCgCgTCAgAATCTgggCACggTTCTgg	
For 3' CTLA-4 amplification		51	GCCCTTGGGCCGGGAGATGGTCTGCTTCAGTGGCGAGGGCAGGTCTGTGTG	ribosomal display 1
For 3' CTLA-4 amplification		49	CGAGGGCAGGTCTGTGTGGGTCACGGTGCACGTGAACCTCTCCCCGGAG	ribosomal display 2
For 3' CTLA-4 amplification		51	CGTGAACCTCTCCCCGGAGTTCCAGTCATCCTCGCAGATGCTGGCCTCACC	ribosomal display 3
//////////////////////////////////////	//////////	//////	//	//
For CDR1-somatostatin	4585	84	AgCTTTgTgTgTgAgTATgCAgCTggCTgCAAgAATTTCTTCTggAAgACTTTCACATCCTgTgCCACTgAggTCCgggTgACA	forward primer + Som
For CDR3-somatostatin	4586	84	CTgggTACCgTTgCCgATgCCACAggATgTgAAAgTCTTCCAgAAgAAATTCTTgCAgCCAgCCTCCACCTTgCAgATgTAgAg	reverse primer +Som
For CDR1-som-randomisation	4835	75	AgCTTTgTgTgTgAgTATgCAgCTggCTgCAAgAATNNg/TNNg/TNNg/TNNg/TNNg/TNNg/TACATCCTgTgCCACTgAggTC	

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For CDR3-som-randomisation	4836	75	CTgggTACCgTTgCCgATgCCACAggATgTA/CNNA/CNNA/CNNA/CNNA/CNNA/CNNATTCTTgCAgCCAgCCTCCACCTTgCA	
For CDR2 haemagglutinin tag	4766	21	gTAggTTgCCgCACAgACTTC	back primer for splice overlap
For CDR2 haemagglutinin tag	4775	66	gAAgTCTgTgCggCAACCTACCCgTATgACgTTCCggACTACgCCCTAgATgATTCCATCTgCACg	forward primer, tag + overlap
/////////////////////////////////	//////////	//////	//	//////////////////////////////////
For CDR-1 anti-lysozyme	5232	78	gCCAgCTTTgTgTgTgAgTATgCCAgTggCTACACCATCgggCCgTACTgCATgggCgTCCgggTgACAgTgCTTCgg	
For CDR-2 anti-lysozyme	5228	60	TgTgCggCAgCCATCAACATgggCggTggCATCACCTTCCTAgATgATTCCATCTgCACg	Forward
For CDR-2 anti-lysozyme	5229	60	ATCTAggAAggTgATgCCACCgCCCATgTTgATggCTgCCgCACAgACTTCAgTCACCTg	Reverse
For CDR-3 anti-lysozyme	5230	69	CAgCCCgTggCCgCACTCgTAgTAggACgCgTAgATCgTcGAgTCCACCTTgCAgATgTAgAgTCCCgT	
For CDR-3 anti-lysozyme	5231	72	AATCTgggTACCgTTgCCgATgCCggAgTCATAgCCgTACCCTCCCgTggACAgCCCgTggCCgCACTCgTA	
/////////////////////////////////	//////////	//////	//	//////////////////////////////////
For CDR-1 anti-melanoma	5341	78	gCCAgCTTTgTgTgTgAgTATgCCAgTggATTCACCTTCAgTTCCTACgCCATgTCCgTCCgggTgACAgTgCTTCgg	
For CDR-2 anti-melanoma	5338	51	gCCATCTCCggATCCggAggCTCgACCTACCTAgATgATTCCATCTgCACg	Forward
For CDR-2 anti-melanoma	5339	54	gTAggTCgAgCCTCCggATCCggAgATggCTgCCgCACAgACTTCAgTCACCTg	Reverse
For CDR-3 anti-melanoma	5351	69	CACgTCCATgTAgTAgTCTCCCTCCTCgCCgCgCAgTCCCCAgCCCACCTTgCAgATgTAgAgTCCCgT	
For CDR-3 anti-melanoma	5340	51	AATCTgggTACCgTTgCCgATgCCCACgTCCATgTAgTAgTCTCCCTCCTC	
/////////////////////////////////	//////////	//////	//	//////////////////////////////////
CDR1 Randomisation	4483	66	AgCTTTgTgTgTgAgTATgCANNg/TNNg/TNNg/TNNg/TNNg/TNNg/TNNg/TNNg/TgCCACTgAggTCCgggTgACA	forward primer / 8 residue random loop
CDR1 Randomisation	4484	68	CACgTggCCCAgCCTgCTgTggTACTggCCAgCAgCCgAggCATCgCCAgCTTTgTgTgTgAgTATgC	extension primer
CDR1 Randomisation	4254	66	gTgTgTgAgTACgCgTNCNNg/CNNg/CNNg/CNNg/CNNg/CNNg/CTgCNNg/CgCTACTgAggTTCgTgTgACCgTC	forward primer with MluI, AflII sites
CDR1 Randomisation	5449	73	gCCAgCTTTgTgTgTgAgTATgCA(NN^{g}/$_{T}$)$_7$ggCgTCCgggTgACAgTgCTTCggCAgg	

Figure 1 (cont'd)

CDR1 Randomisation	5451	82	gCCAgCTTTgTgTgTgAgTATgCA(NN$^{g}/_{T}$)$_{8}$TgCNN$^{g}/_{T}$ggCgTCCgggTgACAgTgCTTCggCAgg	
CDR1 Randomisation	5452	82	gCCAgCTTTgTgTgTgAgTATgCA(NN$^{g}/_{T}$)$_{2}$($^{T}/_{C}$$^{T}/_{A}$$^{T}/_{C}$)(NN$^{g}/_{T}$)($^{T}/_{C}$$^{T}/_{A}$$^{T}/_{C}$)(NN$^{g}/_{T}$)$_{2}$($^{T}/_{C}$$^{T}/_{A}$$^{T}/_{C}$)TgC(NN$^{g}/_{T}$)ggCgTCC gggTgACAgTgCTTCggCAgg	
CDR1 Randomisation	5450	70	gCCAgCTTTgTgTgTgAgTATgCATCTCCAggC(NN$^{g}/_{T}$)$_{4}$gTCCgggTgACAgTgCTTCggCAgg	
CDR1 Randomisation	5446	70	gCCAgCTTTgTgTgTgAgTATgCATCTCCAggCNN$^{g}/_{T}$TgCNN$^{g}/_{T}$NN$^{g}/_{T}$gTCCgggTgACAgTgCTTCggCAgg	
//////////////////////////////////////	//////////	///////	// //////////////////////	//
CDR2 Randomisation	5447	68	gTgACTgAAgTCTgTgCggCAACCTACNN$^{G}/_{T}$NN$^{G}/_{T}$gggNN$^{G}/_{T}$gAgTTgACCTTCCTAgATgATTCCATCTg	
CDR2 Randomisation	5441	30	gTAggTTgCCgCACAgACTTCAgTCACCtg	
CDR2 Randomisation	5448	68	gTgACTgAAgTCTgTgCggCATgCTACNN$^{G}/_{T}$NN$^{G}/_{T}$gggNN$^{G}/_{T}$gAgTTgACCTTCCTAgATgATTCCATCTg	
CDR2 Randomisation	5442	30	gTAgCATgCCgCACAgACTTCAgTCACCtg	
//////////////////////////////////////	//////////	///////	// //////////////////////	//
CDR3 Randomisation	4482	69	CTgggTACCgTTgCCgATgCCC/ANNC/ANNC/ANNC/ANNC/ANNC/ANNC/ANNC/ANNC/ANNCTCCACC TTgCAgATgTAgAg	reverse primer + 9 residue random loop
CDR3 Randomisation	4275	67	AggTggAA (NNg/C)$_{6}$ TgCNNg/CNNg/CNNg/CNNg/CNNg/CNNg/CNNg/CggCATCggCAACggTAC	forward primer withPstI and KpnI overhangs
CDR3 Randomisation	5470	78	AATCTgggTACCgTTgCCgATgCC ($^{A}/_{C}$NN)$_{10}$ CACCTTgCAgATgTAgAgTCCCgT	
CDR3 Randomisation	5474	93	AATCTgggTACCgTTgCCzgATgCCCAg ($^{A}/_{C}$NN)$_{13}$ CTCCACCTTgCAgATgTAgAgTCCCgT	
CDR3 Randomisation	5471	81	AATCTgggTACCgTTgCCgATgCC ($^{A}/_{C}$NN)$_{4}$ gCA ($^{A}/_{C}$NN)$_{6}$ CACCTTgCAgATgTAgAgTCCCgT	
CDR3 Randomisation	5472	87	AATCTgggTACCgTTgCCgATgCC ($^{A}/_{C}$NN)$_{5}$ gCA ($^{A}/_{C}$NN)$_{7}$ CACCTTgCAgATgTAgAgTCCCgT	
CDR3 Randomisation	5475	99	AATCTgggTACCgTTgCCgATgCC ($^{A}/_{C}$NN)$_{6}$ gCA ($^{A}/_{C}$NN)$_{10}$ CACCTTgCAgATgTAgAgTCCCgT	
CDR3 Randomisation	5473	87	AATCTgggTACCgTTgCCgATgCC ($^{g}/_{A}$$^{T}/_{A}$$^{g}/_{A}$)($^{A}/_{C}$NN)$_{4}$ gCA ($^{A}/_{C}$NN)$_{7}$ CACCTTgCAgATgTAgAgTCCCgT	
//////////////////////////////////////	//////////	///////	// //////////////////////	//
CTLA-4 codon-change	5591	70	ATgCACgTggCCCAgCCTgCTgTggTgCTggCCAgCAgCCgTggCATCgCCAgCTTTgTgTgTgAATATg	
CTLA-4 codon-change	5592	77	gCCAgCTTTgTgTgTgAATATgCgTCTggCTATACCATCggCCCgTACTgCATgggTgTgCgTgTgACCgTgCTg Cg	
CTLA-4 codon-change	5598	54	gTgCgTgTgACCgTgCTgCgTCAggCggATAgCCAggTgACCgAAgTTTgCgCg	
CTLA-4 codon-change	5600	75	CAggTgACCgAAgTTTgCgCggCAgCgATCAACATgggCggTggCATCACCTTCCTggATgATTCCATCTgCA	

Figure 1 (cont'd)

			CC	
CTLA-4 codon-change	5599	66	CAgACCCTggATggTCAggTTCACCTggTTACCgCTggAggTgCCggTgCAgATggAATCATCCAg	
CTLA-4 codon-change	5597	57	CACTTTgCAgATgTACAgACCggTATCCATggCACgCAgACCCTggATggTCAggTT	
CTLA-4 codon-change	5606	66	CAggCCATgACCgCATTCgTAATAAgACgCATAgATggTgCTATCCACTTTgCAgATgTACAgACC	
CTLA-4 codon-change	5607	69	CTgggTACCgTTgCCgATgCCAGAATCgTAgCCATAgCCACCggTggACAggCCATgACCgCATTCgTA	
//	///////////	///////	// //////////////////////	//

[1] All oligonucleotides are described 5' to 3'.

2 N represents combination of the four nucleotides

Figure 1 (cont'd)

Figure 2: Polynucleotide sequence of complete cDNA encoding human CTLA-4 and polypeptide sequence of the VLD of human CTLA-4.

A. Polynucleotide Encoding Human CTLA-4 cDNA

```
ATGGCTTGCC TTGGATTTCA GCGGCACAAG GCTCAGCTGA ACCTGGCTGC CAGGACCTGG CCCTGCACTC TCCTGTTTTT... 80
TCTTCTCTTC ATCCCTGTCT TCTGCAAAGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC CGAGGCATCG... 160
CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG... 240
GTGACTGAAG TCTGTGCGGC AACCTACATG ACGGGGAATG AGTTGACCTT CCTAGATGAT TCCATCTGCA CGGGCACCTC... 320
CAGTGGAAAT CAAGTGAACC TCACTATCCA AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA... 400
TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC CCAGATTTAT GTAATTGATC CAGAACCGTG CCCAGATTCT... 480
GACTTCCTCC TCTGGATCCT TGCAGCAGTT AGTTCGGGGT TGTTTTTTTA TAGCTTTCTC CTCACAGCTG TTTCTTTGAG... 560
CAAAATGCTA AAGAAAAGAA GCCCTCTTAC AACAGGGGTC TATGTGAAAA TGCCCCCAAC AGAGCCAGAA TGTGAAAAGC... 640
AATTTCAGCC TTATTTTATT CCCATCAATT GA                                                    ... 672
```

B. Polypeptide Sequence of Human CTLA-4 VLD

```
1         10         20         30         40         50         60         70         80
MHVAQPAVV LASSRGIASF VCEYASPGKA TEVRVTVLRQ ADSQVTEVCA ATYMMGNELT FLDDSICTGT SSGNQVNLTI

          90         100        110   115
QGLRAMDTGL YICKVELMYP PPYYLGIGNG AQIYV
```

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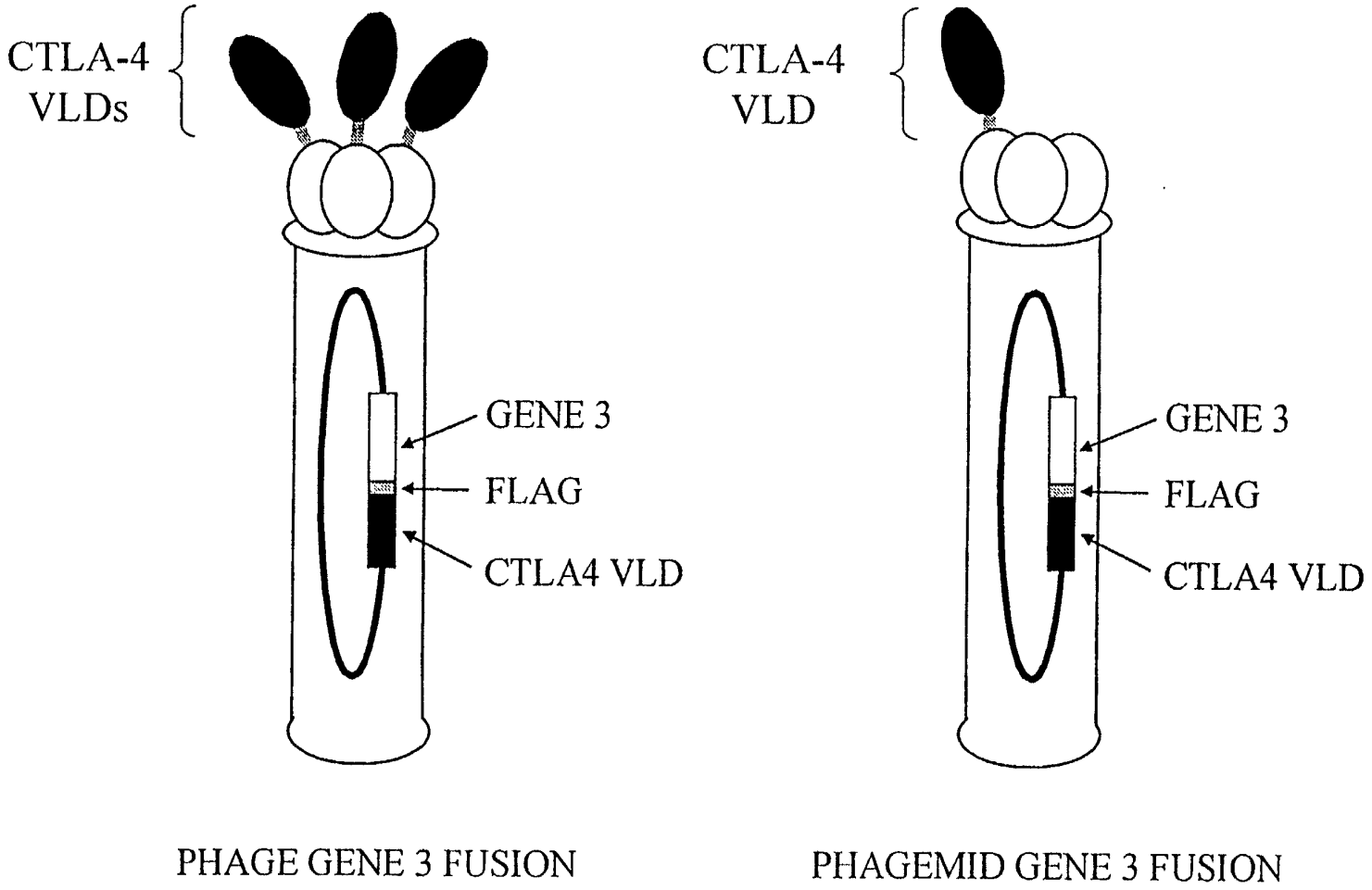
Figure 3: Phage display of CTLA-4 VLD STMs



PHAGE GENE 3 FUSION

PHAGEMID GENE 3 FUSION

Figure 4: Schematic representation of the somatostatin polypeptide.

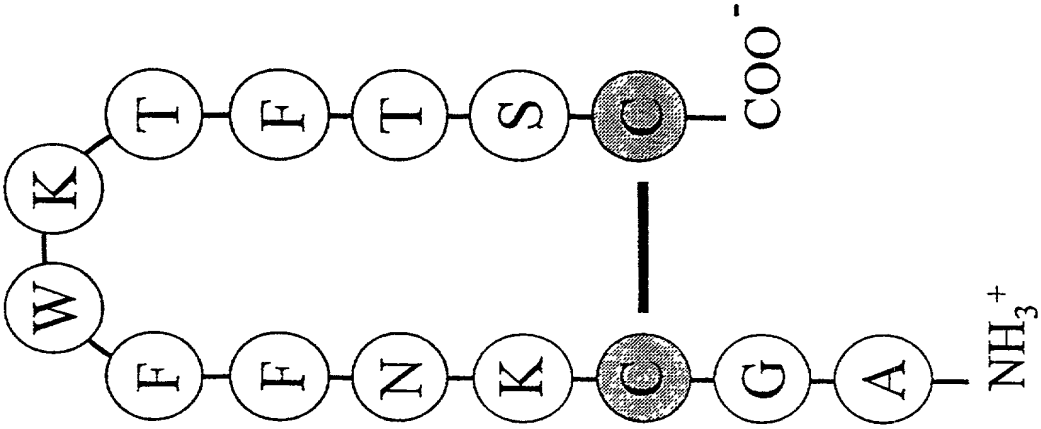


Figure 5: Comparison of the HPLC profiles of affinity purified CTLA-4 VLD and CTLA-4-Som3 STM

Figure 6: Schematic diagram of CTLA-4 VLD CDR loop replacements.

A	CTLA-4 VLD	(S2)	SPGKATE	YMMGNELTF	LMYPPPYYL
B	CTLA-4-Som1	(PP2)	AGCKNFFWKTFTSC	YMMGNELTF	LMYPPPYYL
C	CTLA-4-Som1-Cys120	(PP5)	AGCKNFFWKTFTSC	YMMGNELTF	LMYPPPYYL
D	CTLA-4-Som3	(PP8)	SPGKATE	YMMGNELTF	AGCKNFFWKTFTSC
E	CTLA-4-HA2	(XX4)	SPGKATE	YPYDVPDYA	LMYPPPYYL
F	CTLA-4-Som1-Som3	(VV3)	AGCKNFFWKTFTSC	YMMGNELTF	AGCKNFFWKTFTSC
G	CTLA-4-Som1-HA2-Som3	(ZZ3)	AGCKNFFWKTFTSC	YPYDVPDYA	AGCKNFFWKTFTSC
H	CTLA-4-Anti-Lys	(2V8)	SGYTIGPYCMG	TYMMGNELTF	DSTIYASYYECGHGLSTGGYGYDS
I	CTLA-4-Anti-Mel	(3E4)	SGFTFSSYAMS	AISGSGGSTY	GWGLRGEEGDYYMDV

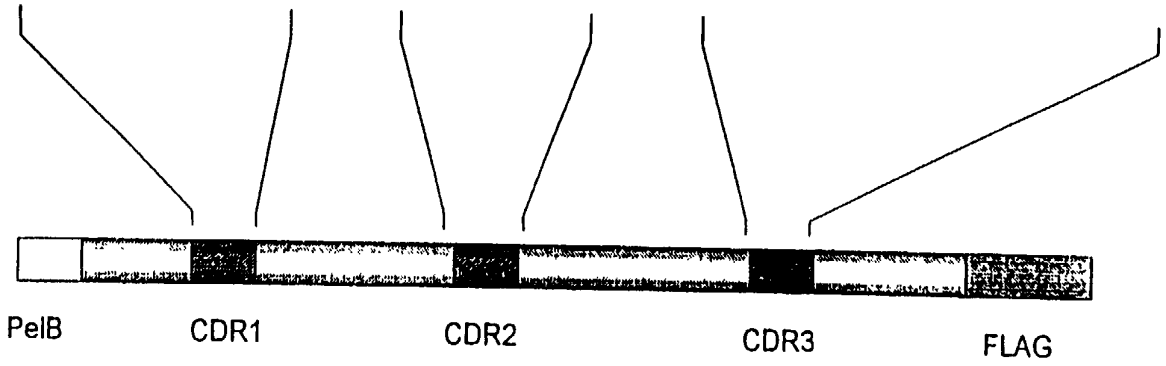


Figure 7: HPLC profiles of affinity purified recombinant CTLA-4 STMs

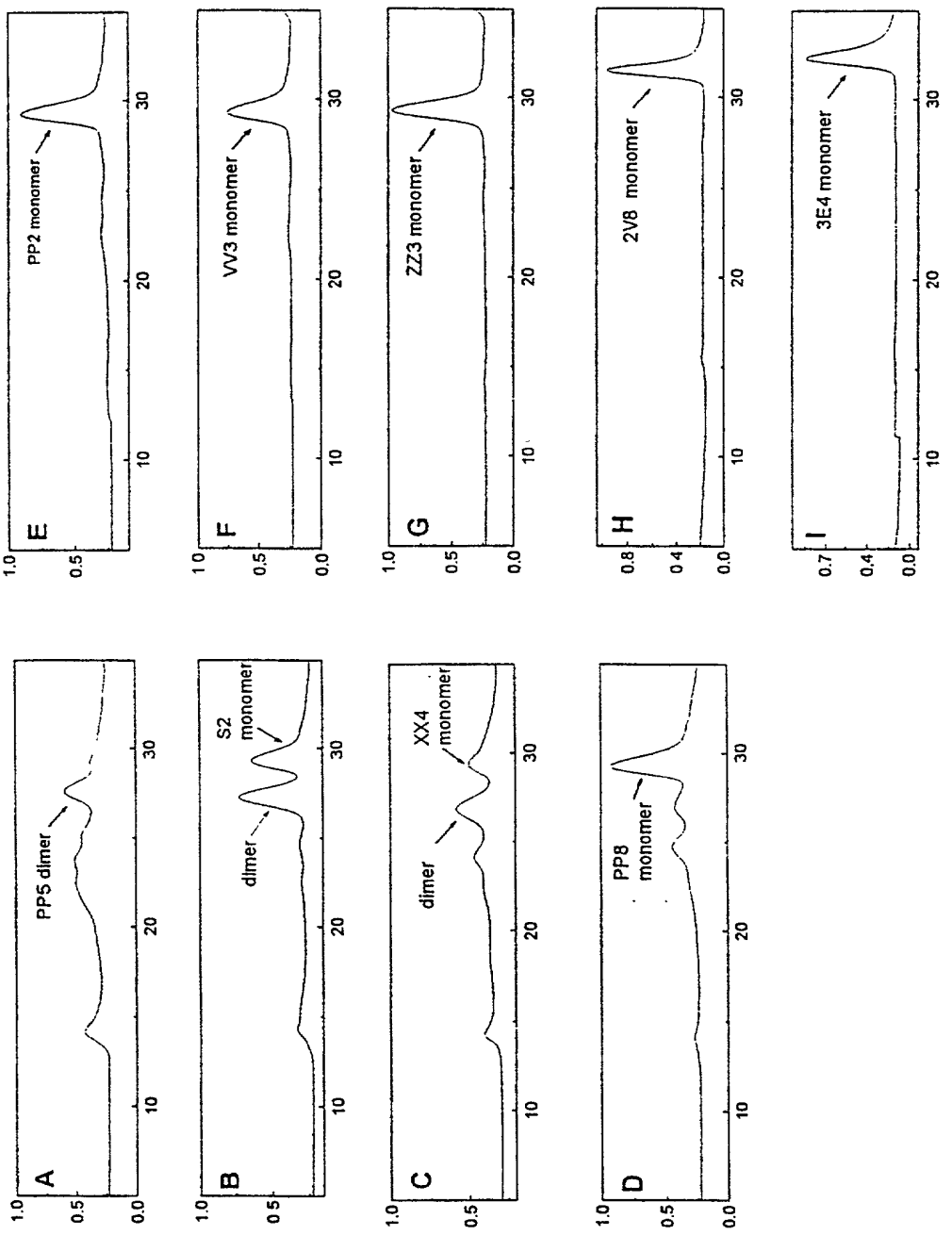


Figure 8: Comparison by size exclusion HPLC analysis of affinity purified CTLA-4 VLD STM constructs synthesised using bacterial expression vector pGC or pPOW.

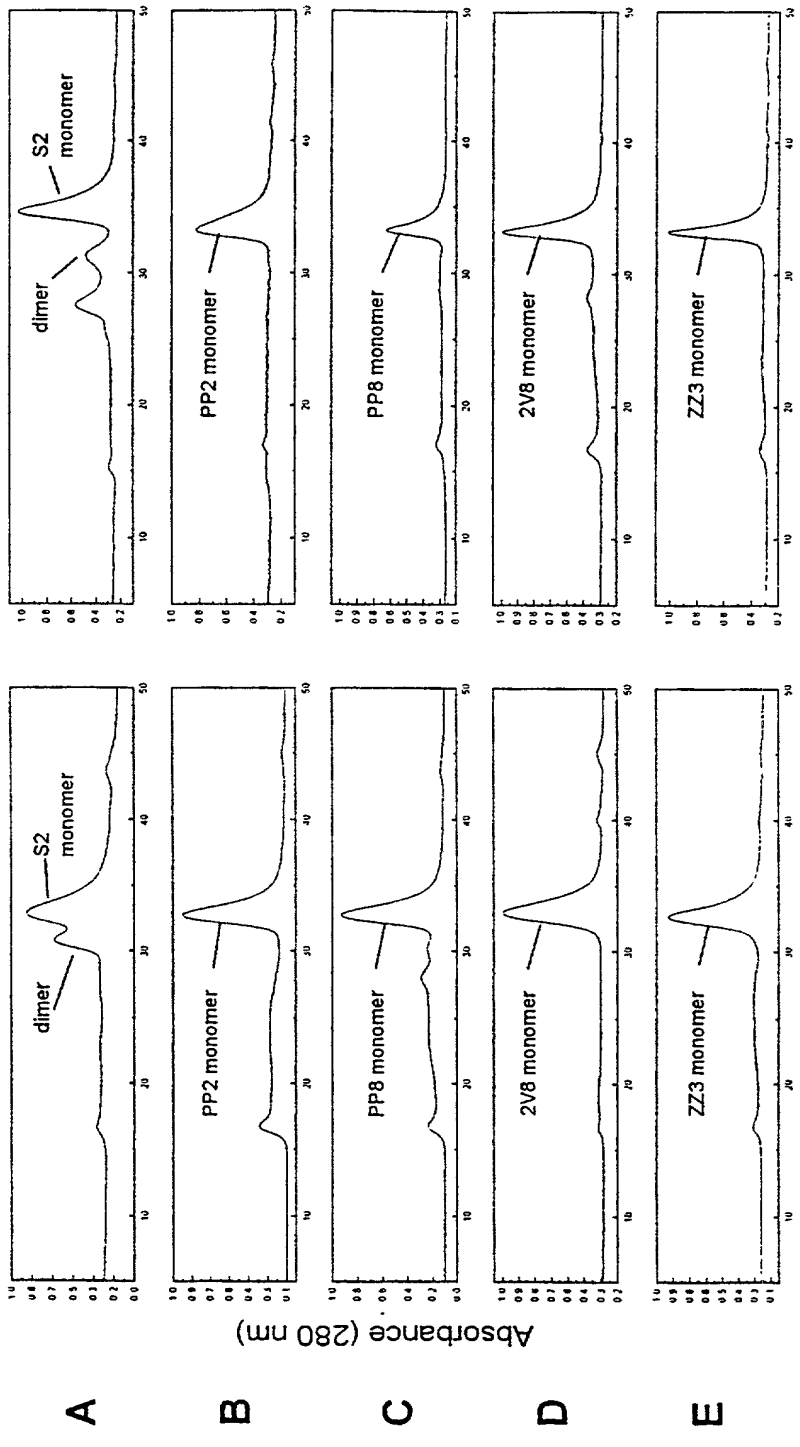


Figure 9: Size exclusion HPLC analysis of affinity purified CTLA-4 VLD STMs: Effect of Freeze/Thaw upon protein

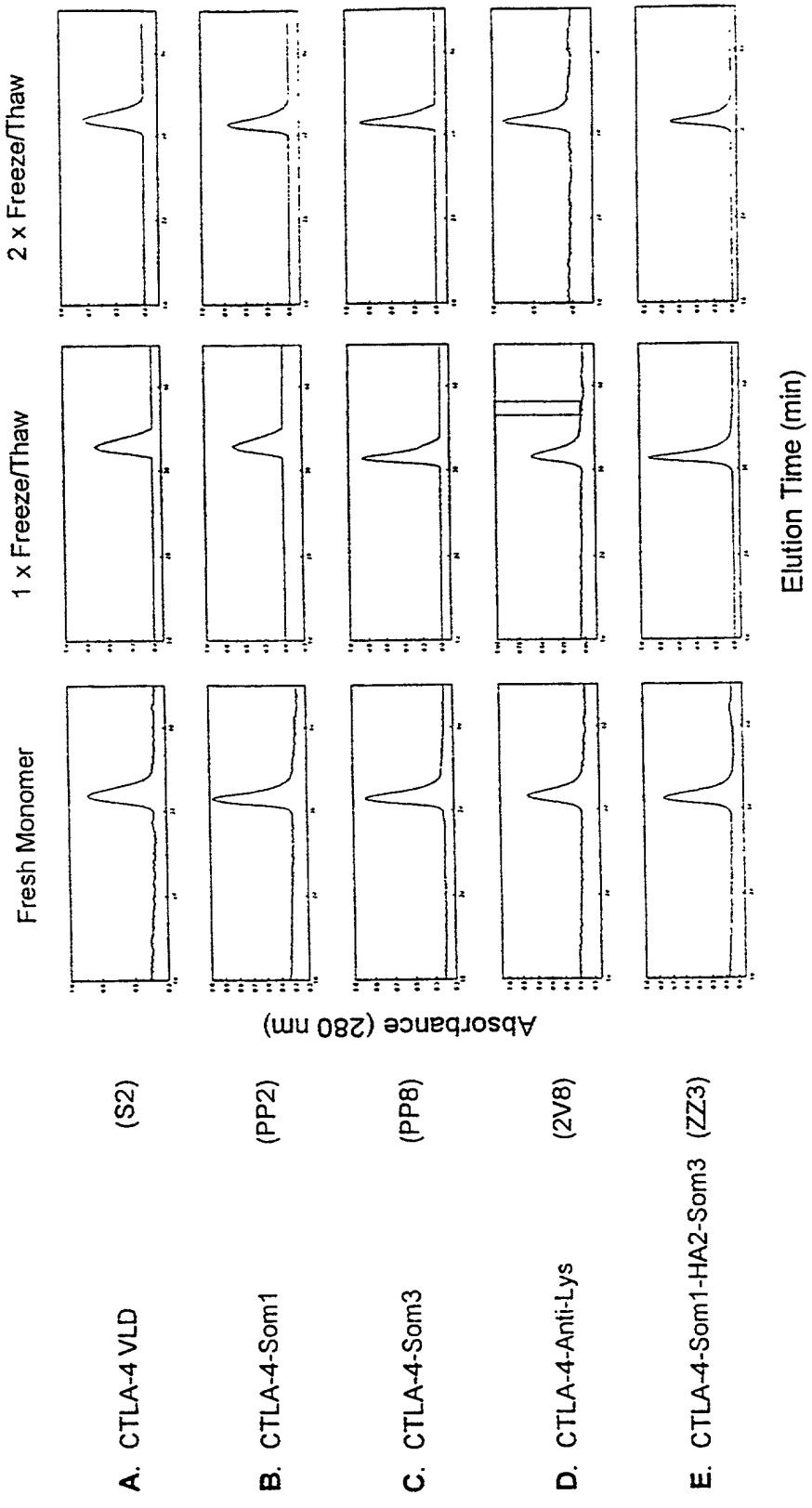


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Figure 10: Lysozyme binding characteristics of CTLA-4 anti-lysozyme construct 2V8

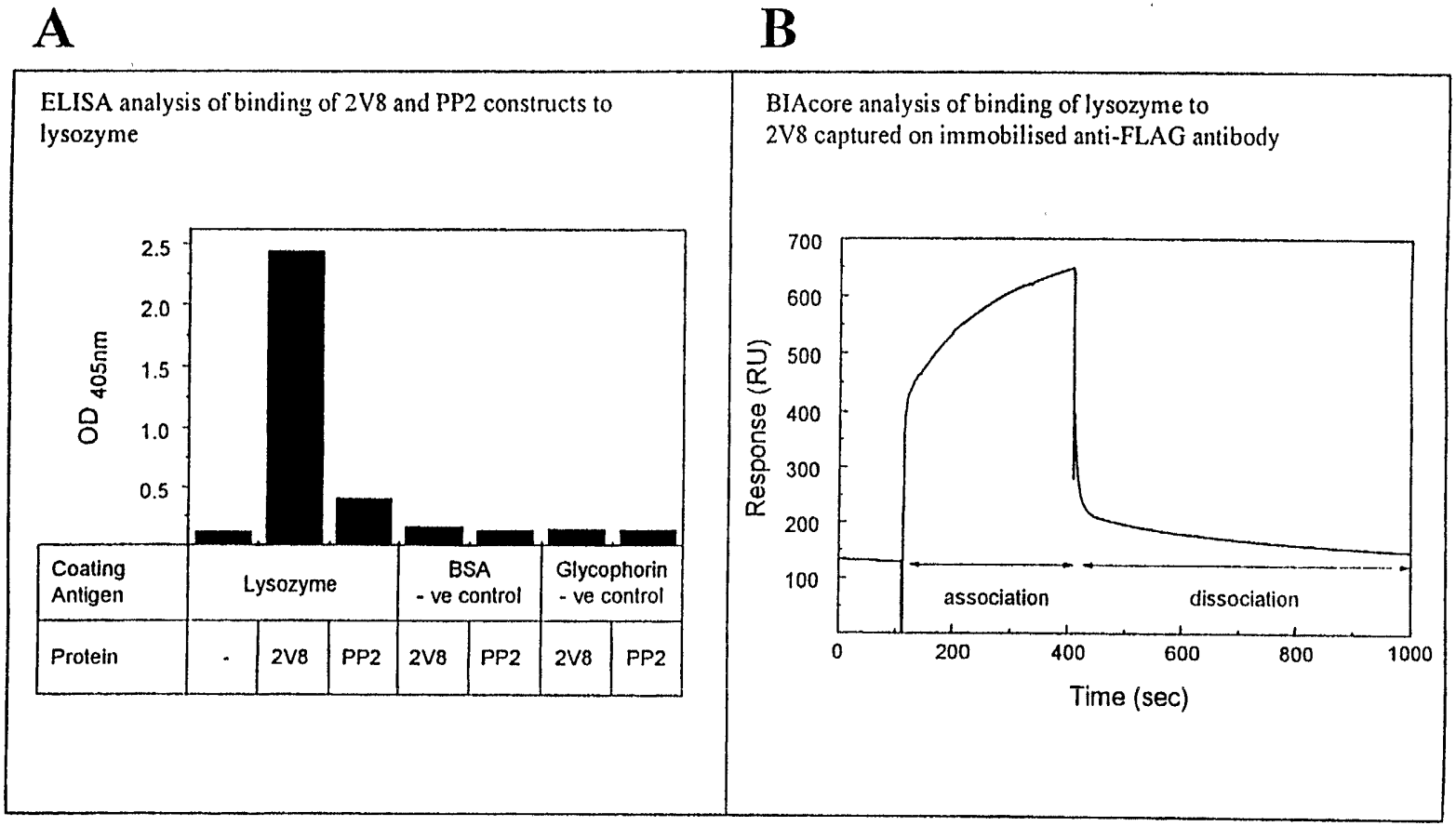


Figure 11: Screening of CTLA-4 VLD Phagemid Library on Immobilised Sh Bleomycin

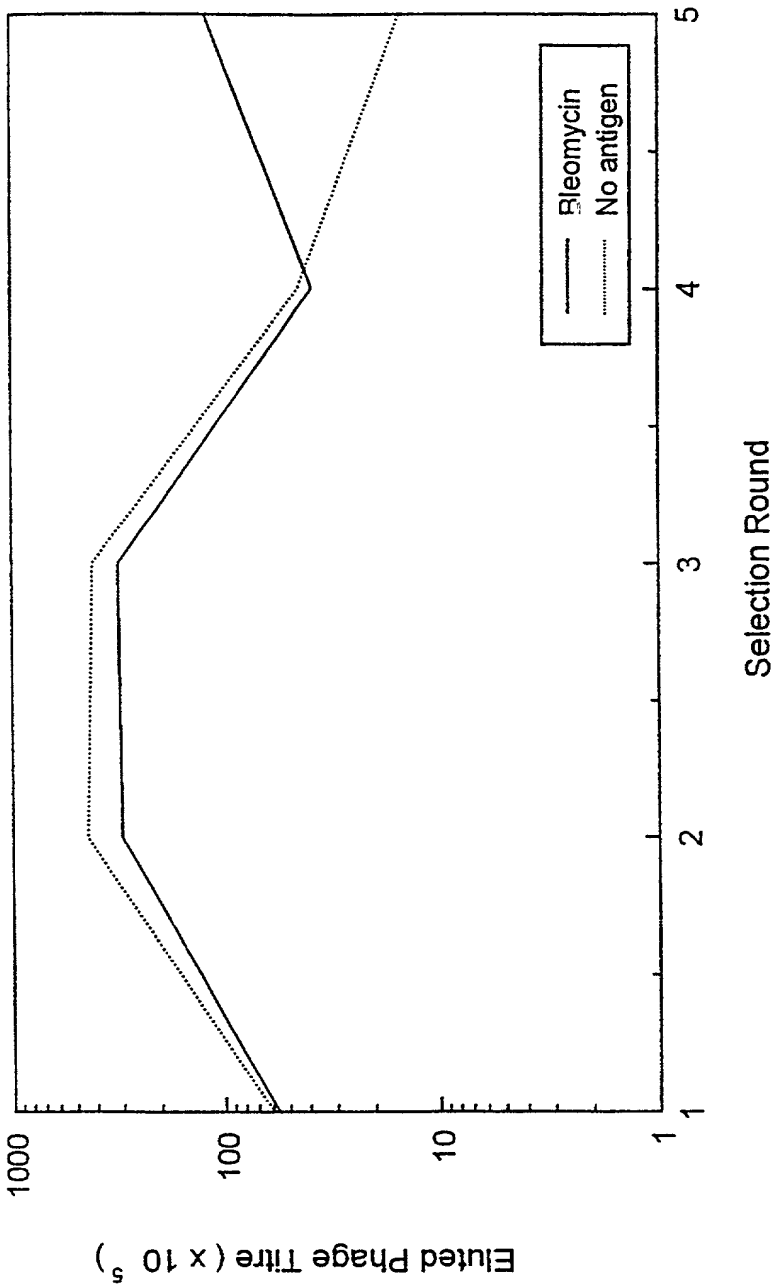
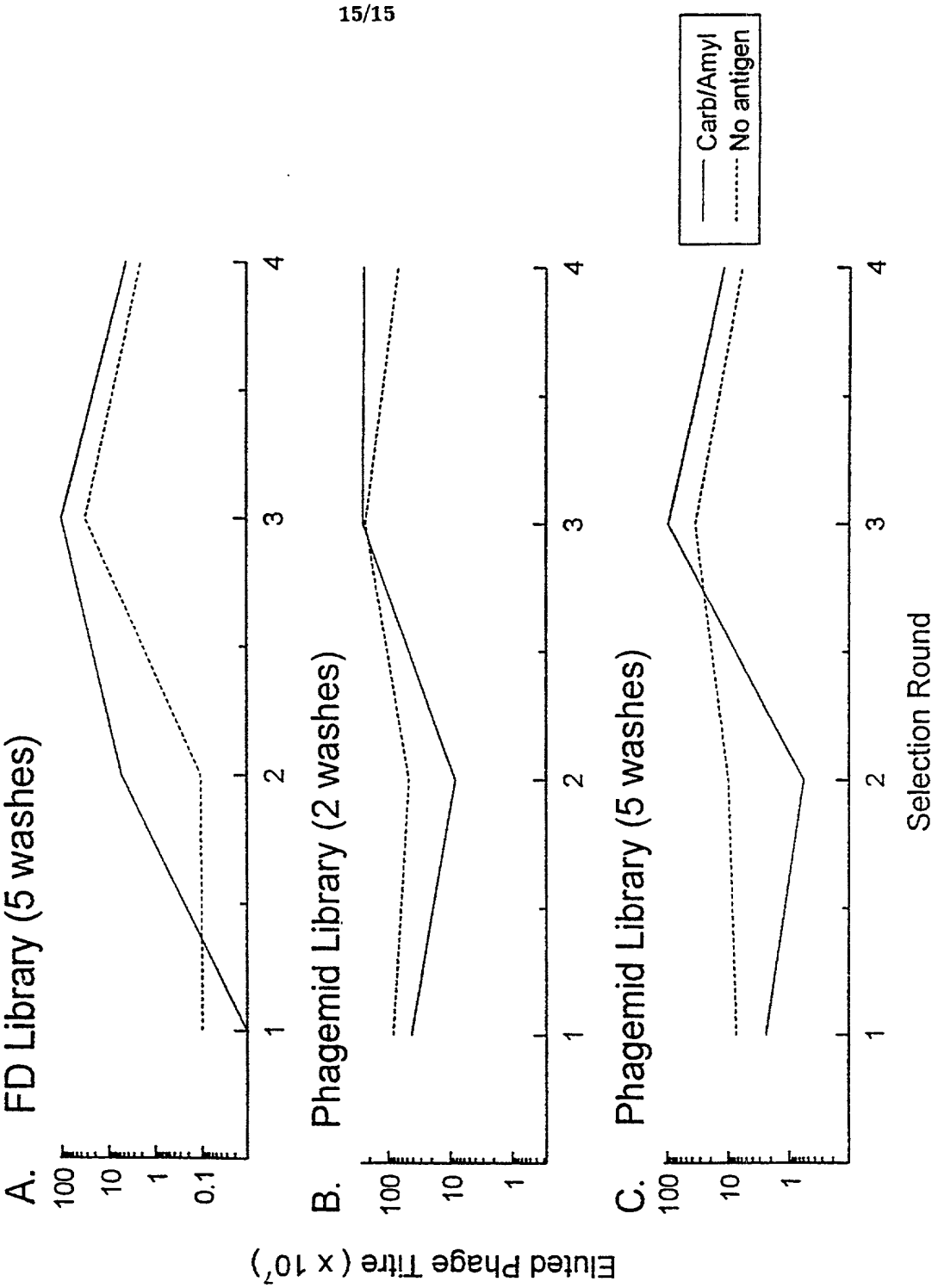


Figure 12: Screening of CTLA-4 VLD libraries in solution.



FLH Docket No.

DECLARATION FOR PATENT APPLICATION AND POWER OF ATTORNEY

(includes reference to PCT International Applications)

FROMMER LAWRENCE & HAUG LLP

As below named inventors, we each hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

We believe we are the original inventors (if plural, names are listed below) of. the subject matter which is claimed and for which a patent is sought on the invention ENTITLED:

V-LIKE DOMAIN BINDING MOLECULES

the specification of which:

is attached hereto

X was filed on SEPTEMBER 5, 2000 as United States of America Serial No. 09/623,611

As the national phase of PCT Application No. PCT/AU99/00136, filed MARCH 5, 1999 designating the US and published as WO 99/45110 on 10 September 1999,

X with amendments through DATE EVEN HEREWITH (if applicable, give details),

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code § 119 (a) - (d) or § 365 (b) of any foreign application(s) for patent or inventor's certificate, or § 365 (a) of any PCT International application(s) designating at least one country other than the United State of America listed below and have also identified below any foreign application for patent or inventor's certificate or any PCT International applications designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) on which priority is claimed:

Prior Foreign/PCT Application(s) [list additional applications on separate page]:

Country (or PCT)	Application Number:	Filed (Day/Month/Year)	Priority Claimed: Yes	No
Australia	PP2210	6 March 1998	X	

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application listed below.

_____ (Application Number) (Filing Date)

FLH Docket No.

I hereby claim the benefit under Title 35, United States Code § 120 of any United States application(s) or § 365 (c) of any PCT international application(s) designating the United States of America that is/are listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in that/those prior United States or PCT International application(s) in the manner provided by the first paragraph of Title 35, United States Code § 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application:

Prior U.S. (or U.S.-designating PCT) Application(s) [list additional applications on separate page]:

U.S. Serial No.:	Filed (Day/Month/Year)	PCT Application No.	Status (patented, pending, abandoned)
PCT	5 March 1999	PCT/AU99/00136	Pending (this application is the National Phase of the PCT)

I hereby appoint Thomas J. Kowalski, Registration No. 32,147, and FROMMER LAWRENCE & HAUG, LLP or their duly appointed associates, my attorneys or agents, with full power of substitution and revocation, to prosecute this application, to make alterations and amendments therein, to file continuation and divisional applications thereof, to receive the Patent, and to transact all business in the Patent and Trademark Office and in the Courts in connection therewith, and to insert the Serial Number of the application in the space provided above, and specify that all communications about the application are to be directed to the following correspondence address:

Thomas J. Kowalski, Esq.
c/o FROMMER LAWRENCE & HAUG, LLP
745 Fifth Avenue
New York, NY 10151
FAX (212) 588-0500

Direct all telephone calls to: (212) 588-0800
to the attention of:
Thomas J. Kowalski

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that wilful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such wilful false statements may jeopardize the validity of the application or any patent issued thereon.

INVENTOR(S):

Signature: _____ Date: 3/8/00

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AUX

FLH Docket No.

Signature: _____ Date: 11/9/2000

2nd

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3rd

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4th

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Signature: _____ Date: 31/8/00.

5th

Full name of fifth joint inventor: **Stewart Douglas NUTTALL**
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Citizenship: Australia

Signature: _____ Date: _____

Post Office Address(es) of inventors [if different from residence]: